

OM protein - protein search, using sw model  
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 GenCore version 5.1.9

## SUMMARIES

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OM protein - protein search, using sw model

Run on: August 14, 2006, 21:51:58 ; Search time 49 Seconds  
(w/o alignments)  
239,369 Million cell updates/sec

Title: Perfect score: US-10-735-149-28  
Sequence: RGQDRHMRQLIDIVDQ.....LQKQHQLSRSRGS 134.  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591.

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/5\_COMB.pep: \*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/6\_COMB.pep: \*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/7\_COMB.pep: \*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/H\_COMB.pep: \*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/PCTUS\_COMB.pep: \*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/RB\_COMB.pep: \*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description           |
|------------|-------|--------------------|-------|-----------------------|
| 1          | 705   | 99.3               | 162   | 2 US-09-522-217-2     |
| 2          | 706   | 99.3               | 162   | 2 US-09-523-216-2     |
| 3          | 706   | 99.3               | 162   | 2 US-10-295-723-2     |
| 4          | 705   | 99.3               | 162   | 2 US-09-825-561A-10   |
| 5          | 706   | 99.3               | 162   | 2 US-10-382-622-2     |
| 6          | 705   | 99.3               | 174   | 2 US-09-949-016-10307 |
| 7          | 695   | 97.7               | 159   | 2 US-09-522-217-85    |
| 8          | 695   | 97.7               | 159   | 2 US-09-23-246-85     |
| 9          | 695   | 97.7               | 159   | 2 US-10-295-723-85    |
| 10         | 694   | 97.6               | 162   | 2 US-10-282-622-6     |
| 11         | 621   | 87.3               | 147   | 2 US-10-382-622-4     |
| 12         | 404   | 56.8               | 146   | 2 US-09-522-217-56    |
| 13         | 404   | 56.8               | 146   | 2 US-09-923-246-55    |
| 14         | 404   | 56.8               | 146   | 2 US-10-395-723-56    |
| 15         | 404   | 56.8               | 146   | 2 US-09-825-561A-47   |
| 16         | 394   | 55.4               | 510   | 2 US-09-522-217-89    |
| 17         | 394   | 55.4               | 510   | 2 US-10-295-723-89    |
| 18         | 394   | 55.4               | 510   | 2 US-09-522-217-72    |
| 19         | 212   | 29.8               | 40    | 2 US-09-923-246-72    |
| 20         | 212   | 29.8               | 40    | 2 US-10-295-723-72    |
| 21         | 212   | 29.8               | 40    | 2 US-10-295-723-72    |
| 22         | 176   | 24.8               | 32    | 2 US-09-522-217-73    |
| 23         | 176   | 24.8               | 32    | 2 US-09-923-246-73    |
| 24         | 176   | 24.8               | 32    | 2 US-10-295-723-73    |
| 25         | 99.5  | 14.0               | 114   | 1 US-09-031-339-5     |
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ALIGNMENTS

RESULT 1  
US-09-522-217-2

Sequence 2, Application US/09522217  
Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: E. PRESNELL, SCOTT R.

APPLICANT: SPRECHER, CINDY A.

APPLICANT: FOSTER, DONALD C.

APPLICANT: HOLLY, RICHARD D.

APPLICANT: GROSS, JANE A.

APPLICANT: JOHNSON, JANET V.

APPLICANT: NELSON, ANDREW J.

APPLICANT: DILLON, STACEY R.

APPLICANT: HAMMOND, ANGELA K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPH1 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: US 60/123,904

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0

SEQ ID NO 2

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-522-217-2

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Best Local Similarity: 100.0%; Pred. No. 5.4e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 89, Appl. Db 30 QGDQRHMRQLIDIVDQKVNNDLVERFLPAPDVETNCWASRPSFCQKQAKLSANT 89

Sequence 89, Appl. Qy 62 GNNERIINVSIKKRKPKSTNAGERRQKRLTCSCDSYEKKPPEPLERKSLQKMH 121  
Sequence 72, Appl. Db 90 GNNERIINVSIKKRKPKSTNAGERRQKRLTCSCDSYEKKPPEPLERKSLQKMH 149

Sequence 72, Appl. Sequence 73, Appl. Qy 122 QHSRSRTGS 134  
Sequence 73, Appl. Sequence 73, Appl. Db 150 QHSRSRTGS 162

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OM protein - protein search, using sw model  
GenCore version 5.1.9

Run on: August 14, 2006, 21:51:58 : Search time 49 Seconds  
239.369 Million cell updates/sec

Title: US-10-735-149-28  
Perfect score: 711  
Sequence: 1 MQGQDRMIRMRQLIDVQD.....LLQRMWIMHQIHSSTRHGSBDS 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 65591 seqs, 8753628 residues

Total number of hits satisfying chosen parameters: 650591  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

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|----|---|
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| 2: | /EMC_Celerra_SIDS3/ptodata/2/1aa/6_COMB.pep:*       |
| 3: | /EMC_Celerra_SIDS3/ptodata/2/1aa/7_COMB.pep:*       |
| 4: | /EMC_Celerra_SIDS3/ptodata/2/1aa/H_COMB.pep:*       |
| 5: | /EMC_Celerra_SIDS3/ptodata/2/1aa/L_PCTUS_COMB.pep:* |
| 6: | /EMC_Celerra_SIDS3/ptodata/2/1aa/R_R_COMB.pep:*     |
| 7: | /EMC_Celerra_SIDS3/ptodata/2/1aa/bacffiles1.pep:*   |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| Result No. | Score | Query Match length | DB ID | Description                            |
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| 1          | 706   | 99.3               | 162   | 2 US-09-522-217-2 Sequence 2, Appli    |
| 2          | 706   | 99.3               | 162   | 2 US-09-923-246-2 Sequence 2, Appli    |
| 3          | 706   | 99.3               | 162   | 2 US-10-295-723-2 Sequence 2, Appli    |
| 4          | 706   | 99.3               | 162   | 2 US-09-825-561A-10 Sequence 2, Appli  |
| 5          | 706   | 99.3               | 162   | 2 US-10-282-622-2 Sequence 2, Appli    |
| 6          | 705   | 99.3               | 174   | 2 US-09-949-016-0307 Sequence 103, A   |
| 7          | 695   | 97.7               | 519   | 2 US-09-522-217-85 Sequence 85, Appli  |
| 8          | 695   | 97.7               | 519   | 2 US-09-923-246-85 Sequence 85, Appli  |
| 9          | 695   | 97.7               | 519   | 2 US-10-295-723-85 Sequence 85, Appli  |
| 10         | 694   | 97.6               | 162   | 2 US-09-825-561A-10 Sequence 6, Appli  |
| 11         | 621   | 87.3               | 147   | 2 US-10-282-622-4 Sequence 4, Appli    |
| 12         | 404   | 56.8               | 146   | 2 US-09-522-217-56 Sequence 56, Appli  |
| 13         | 404   | 56.8               | 146   | 2 US-09-923-246-56 Sequence 56, Appli  |
| 14         | 404   | 56.8               | 146   | 2 US-10-295-723-56 Sequence 56, Appli  |
| 15         | 404   | 56.8               | 146   | 2 US-09-825-561A-47 Sequence 47, Appli |
| 16         | 394   | 55.4               | 510   | 2 US-09-522-217-89 Sequence 89, Appli  |
| 17         | 394   | 55.4               | 510   | 2 US-09-923-246-89 Sequence 89, Appli  |
| 18         | 394   | 55.4               | 510   | 2 US-10-295-723-89 Sequence 89, Appli  |
| 19         | 212   | 29.8               | 40    | 2 US-09-522-217-72 Sequence 72, Appli  |
| 20         | 212   | 29.8               | 40    | 2 US-09-923-246-72 Sequence 72, Appli  |
| 21         | 212   | 29.8               | 40    | 2 US-10-295-723-72 Sequence 72, Appli  |
| 22         | 212   | 24.8               | 32    | 2 US-09-522-217-73 Sequence 73, Appli  |
| 23         | 176   | 24.8               | 32    | 2 US-09-923-246-73 Sequence 73, Appli  |
| 24         | 176   | 24.8               | 32    | 2 US-10-295-723-73 Sequence 73, Appli  |
| 25         | 99.5  | 14.0               | 114   | 1 US-09-522-217-73 Sequence 6, Appli   |
| 26         | 99.5  | 14.0               | 114   | 1 US-09-031-399-6 Sequence 12, Appli   |

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| 27 | 99.5 | 14.0 | 114 | 1 | US-08-393-305-3   | Sequence 3, Appli  |
| 28 | 99.5 | 14.0 | 114 | 1 | US-08-726-817-3   | Sequence 3, Appli  |
| 29 | 99.5 | 14.0 | 114 | 1 | US-08-504-042-6   | Sequence 6, Appli  |
| 30 | 99.5 | 14.0 | 114 | 1 | US-08-504-042-12  | Sequence 12, Appli |
| 31 | 99.5 | 14.0 | 114 | 1 | US-08-725-969-3   | Sequence 3, Appli  |
| 32 | 99.5 | 14.0 | 114 | 1 | US-08-794-524-3   | Sequence 3, Appli  |
| 33 | 99.5 | 14.0 | 114 | 2 | US-08-189-193-3   | Sequence 3, Appli  |
| 34 | 99.5 | 14.0 | 114 | 2 | US-09-462-941-20  | Sequence 20, Appli |
| 35 | 99.5 | 14.0 | 114 | 5 | PCT-US94-03793-6  | Sequence 6, Appli  |
| 36 | 99.5 | 14.0 | 114 | 5 | PCT-US94-03793-12 | Sequence 12, Appli |
| 37 | 99.5 | 14.0 | 162 | 1 | US-08-031-399-5   | Sequence 5, Appli  |
| 38 | 99.5 | 14.0 | 162 | 1 | US-08-393-305-2   | Sequence 2, Appli  |
| 39 | 99.5 | 14.0 | 162 | 1 | US-08-535-733-2   | Sequence 2, Appli  |
| 40 | 99.5 | 14.0 | 162 | 1 | US-08-726-817-2   | Sequence 2, Appli  |
| 41 | 99.5 | 14.0 | 162 | 1 | US-08-504-042-5   | Sequence 5, Appli  |
| 42 | 99.5 | 14.0 | 162 | 1 | US-08-725-969-2   | Sequence 2, Appli  |
| 43 | 99.5 | 14.0 | 162 | 1 | US-08-794-524-2   | Sequence 2, Appli  |
| 44 | 99.5 | 14.0 | 162 | 2 | US-08-842-947-6   | Sequence 6, Appli  |
| 45 | 99.5 | 14.0 | 162 | 2 | US-08-189-193-2   | Sequence 2, Appli  |

RESULT 2  
US-09-923-246-2  
; Sequence 2, Application US/09923246  
; Patent No. 6605272  
; GENERAL INFORMATION:  
; APPLICANT: No. 6605272ak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/09/923,246  
; PRIORITY FILING DATE: 2001-08-03  
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217  
; PRIORITY FILING DATE: 2000-03-09  
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904  
; PRIORITY FILING DATE: EARLIER FILING DATE: 1999-03-11  
; PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013  
; PRIORITY FILING DATE: EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-923-246-2  
Query Match 99.3%; Score 706; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.4e-73; Mismatches 0; Indels 0; Gaps 0;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 30 QGODRHMIRMRQLDIDVQQLKVNNDIVLUPEFLPAPEDVETNECEWSAFAFSCFOKAQLKSANT 89  
Qy 62 GNNERIINVISIKLKRRKPPSTNAGRRQKRHLTCPSCDSYEKKPKPLERFLKSLQKMH 121  
Db 90 GNNERIINVISIKLKRRKPPSTNAGRRQKRHLTCPSCDSYEKKPKPLERFLKSLQKMH 149  
Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

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RESULT 4  
US-09-825-561A-10  
; Sequence 10, Application US/09825561A  
; Patent No. 6777539  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; TITLE OF INVENTION: SOLUBLE ZALPHALL CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22  
; CURRENT APPLICATION NUMBER: US/09/825,561A  
; CURRENT FILING DATE: 2000-04-05  
; PRIORITY APPLICATION NUMBER: US 60/194,731  
; PRIORITY FILING DATE: 2000-04-05  
; PRIORITY APPLICATION NUMBER: US 60/222,121  
; PRIORITY FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-825-561A-10  
Query Match 99.3%; Score 706; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.4e-73; Mismatches 0; Indels 0; Gaps 0;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 30 QGODRHMIRMRQLDIDVQQLKVNNDIVLUPEFLPAPEDVETNECEWSAFAFSCFOKAQLKSANT 89  
Qy 62 GNNERIINVISIKLKRRKPPSTNAGRRQKRHLTCPSCDSYEKKPKPLERFLKSLQKMH 121  
Db 90 GNNERIINVISIKLKRRKPPSTNAGRRQKRHLTCPSCDSYEKKPKPLERFLKSLQKMH 149

RESULT 5  
 US-10-822-622-2  
 Sequence 2, Application US/10282622  
 Patent No. 692992  
 GENERAL INFORMATION:  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: West, James W.  
 ; TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS  
 ; CURRENT APPLICATION NUMBER: US/10/282,622  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIORITY NUMBER: 60/337,586  
 ; PRIORITY FILING DATE: 2001-11-05  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-282-622-2

Query Match

Best Local Similarity 100.0%; Score 706; DB 2; Length 162;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGDGRHMRMQLDIVDQLKNTNDLVPEFLPAPEDVETNCWSAFCFOQAKLSANT 61  
 Db 30 QGDGRHMRMQLDIVDQLKNTNDLVPEFLPAPEDVETNCWSAFCFOQAKLSANT 89  
 Qy 62 GNNERITIVNSIKUKRKPSTNAGRRQKRHLTCPSDCDSYEKKKPKEPLRFKSLLQMH 121  
 Db 90 GNNERITIVNSIKUKRKPSTNAGRRQKRHLTCPSDCDSYEKKKPKEPLRFKSLLQMH 149  
 Qy 122 QHLSRSRTGSEDS 134  
 Db 150 QHLSRSRTGSEDS 162

RESULT 6  
 US-09-949-016-10307

Sequence 10307, Application US/09949016

GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL0101307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIORITY NUMBER: 60/241,755  
 ; PRIORITY FILING DATE: 2000-10-20  
 ; PRIORITY APPLICATION NUMBER: 60/237,768  
 ; PRIORITY FILING DATE: 2000-10-03  
 ; PRIORITY APPLICATION NUMBER: 60/231,498  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 10307  
 ; LENGTH: 174  
 ; TYPE: PRT  
 ; ORGANISM: Human

Query Match

Best Local Similarity 99.3%; Score 706; DB 2; Length 174;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-949-016-10307

RESULT 7  
 US-09-522-217-85

Sequence 85, Application US/09522217

GENERAL INFORMATION:

; APPLICANT: No. 6307024ak, Julia E.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.

; APPLICANT: Nelson, Andrew J.

; APPLICANT: Dillon, Stacey R.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND

; FILE REFERENCE: 99-16-217

; CURRENT APPLICATION NUMBER: US/09/522,217

; EARLIER APPLICATION NUMBER: US 60/123,547

; EARLIER FILING DATE: 1999-03-09

; EARLIER APPLICATION NUMBER: US 60/142,013

; EARLIER FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 85

; LENGTH: 519

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE: OTHER INFORMATION: MBP-human zalphal1 Ligand fusion polypeptide

US-09-522-217-85

Query Match

Best Local Similarity 100.0%; Score 695; DB 2; Length 519;

Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QDGRHMRMQLDIVDQLKNTNDLVPEFLPAPEDVETNCWSAFCFOQAKLSANTGN 63  
 Db 389 QDGRHMRMQLDIVDQLKNTNDLVPEFLPAPEDVETNCWSAFCFOQAKLSANTGN 448  
 Qy 64 NERINIVNSIKUKRKPSTNAGRRQKRHLTCPSDCDSYEKKKPKEPLRFKSLLQMHQ 123  
 Db 449 NERINIVNSIKUKRKPSTNAGRRQKRHLTCPSDCDSYEKKKPKEPLRFKSLLQMHQ 508  
 Qy 124 LSRSRTGSEDS 134  
 Db 509 LSRSRTGSEDS 519

RESULT 8  
 US-09-923-246-85

Sequence 85, Application US/09923246

GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.

; APPLICANT: Nelson, Andrew J.

; APPLICANT: Johnston, Janet V.

; TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS  
 ; CURRENT APPLICATION NUMBER: US/10/282,622  
 ; CURRENT FILING DATE: 2002-10-28  
 ; PRIORITY NUMBER: 60/337,586  
 ; PRIORITY FILING DATE: 2001-11-05  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0

Query Match

Best Local Similarity 100.0%; Score 706; DB 2; Length 174;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGDGRHMRMQLDIVDQLKNTNDLVPEFLPAPEDVETNCWSAFCFOQAKLSANT 61  
 Db 42 QGDGRHMRMQLDIVDQLKNTNDLVPEFLPAPEDVETNCWSAFCFOQAKLSANT 101

APPLICANT: Nelson, Andrew J.  
 APPLICANT: Dillon, Stacey R.  
 APPLICANT: Hammond, Angela K.  
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI1 LIGAND  
 FILE REFERENCE: 99-16  
 CURRENT APPLICATION NUMBER: US/09/923, 246  
 CURRENT FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522, 217  
 PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123, 904  
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142, 013  
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
 NUMBER OF SEQ ID NOS: 115  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 85  
 LENGTH: 519  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: MBP-human zalphai1 Ligand fusion polypeptide  
 US-09-923-246-85  
 Query Match 97.7%; Score 695; DB 2; Length 519;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-71;  
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 QDRHMIRNQLDIDVQKNYNDLVREFLPAPEDVETNCNSAFSCFQKQQLKSANTGN 63  
 Db 389 QDRHMIRNQLDIDVQKNYNDLVREFLPAPEDVETNCNSAFSCFQKQQLKSANTGN 448  
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 Db 449 NERIINVSIKLUKRKPSTNAGRRQKRHLTCPSDCSYEKKPKFPLRFKSLIQKMTHQH 508  
 Qy 124 LSRRTHSEDS 134  
 Db 509 LSRRTHSEDS 519  
 RESULT 9  
 US-10-295-723-85  
 Sequence 85, Application US/10295723  
 Patent No. 6686178  
 GENERAL INFORMATION:  
 APPLICANT: Presnell, Scott R.  
 APPLICANT: West, James W.  
 APPLICANT: No. 622932ak, Julia E.  
 TITLE OF INVENTION: ZALPHAI1 LIGAND ANTAGONISTS  
 FILE REFERENCE: 01-37  
 CURRENT APPLICATION NUMBER: US/10/282, 622  
 CURRENT FILING DATE: 2002-10-28  
 PRIOR APPLICATION NUMBER: 60/337, 586  
 PRIOR FILING DATE: 2001-11-05  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 6  
 LENGTH: 162  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: zalphai1 Ligand Q153D/I156D  
 US-10-282-622-6  
 Query Match 97.6%; Score 694; DB 2; Length 162;  
 Best Local Similarity 98.5%; Pred. No. 1.3e-71; Matches 131; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 QGDRHMIRNQLDIDVQKNYNDLVREFLPAPEDVETNCNSAFSCFQKQQLKSANTGN 61  
 Db 30 QGDRHMIRNQLDIDVQKNYNDLVREFLPAPEDVETNCNSAFSCFQKQQLKSANT 89  
 Qy 62 GNNERIINVSIKLUKRKPSTNAGRRQKRHLTCPSDCSYEKKPKFPLRFKSLIQKMTH 121  
 Db 90 GNNERIINVSIKLUKRKPSTNAGRRQKRHLTCPSDCSYEKKPKFPLRFKSLIQKMTH 149  
 Qy 122 QHSRRTHSEDS 134  
 Db 150 QHSRRTHSEDS 162  
 RESULT 11  
 US-10-282-622-4  
 Sequence 4, Application US/10282622  
 Patent No. 629932  
 GENERAL INFORMATION:  
 APPLICANT: Presnell, Scott R.  
 APPLICANT: West, James W.  
 APPLICANT: No. 622932ak, Julia E.  
 TITLE OF INVENTION: ZALPHAI1 LIGAND ANTAGONISTS  
 FILE REFERENCE: 01-37  
 CURRENT APPLICATION NUMBER: US/10/282, 622  
 ;

Db 143 QHLS 146  
 CURRENT FILING DATE: 2002-10-28  
 PRIOR APPLICATION NUMBER: 60/337,586  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 4  
 LENGTH: 147  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 OTHER INFORMATION: zalphall ligand Q153ST/1156D  
 US-10-282-22-4  
 RESULT 13  
 Query Match 87.3%; Score 621; DB 2; Length 147;  
 Best Local Similarity 99.2%; Pred. No. 2; e=63;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QGDPRHRMIRMRQLIDIVDQKLVNDVPEFLPAPEDVETNEWSAFCFOAKLKSANT 61  
 Db 30 QGDPRHRMIRMRQLIDIVDQKLVNDVPEFLPAPEDVETNEWSAFCFOAKLKSANT 89  
 QY 62 GNNERIINVSIKKRKRPSTNAGRGRKRHRGKPCSDSYEKPPKEFLERFLQMH 119  
 Db 90 GNNERIINVSIKKRKRPSTNAGRGRKRHRGKPCSDSYEKPPKEFLERFLQMH 147  
 RESULT 12  
 ; Sequence 56, Application US/09522217  
 GENERAL INFORMATION:  
 ; APPLICANT: No. 6307024ak, Julia E.  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Sprecher, Cindy A.  
 ; APPLICANT: Foster, Donald C.  
 ; APPLICANT: Holly, Richard D.  
 ; APPLICANT: Gross, Jane A.  
 ; APPLICANT: Johnston, Janet V.  
 ; APPLICANT: Nelson, Andrew J.  
 ; APPLICANT: Dillon, Stacey R.  
 ; APPLICANT: Hammond, Angela K.  
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND  
 FILE REFERENCE: 99-16  
 CURRENT APPLICATION NUMBER: US/09/923,246  
 CURRENT FILING DATE: 2001-08-03  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217  
 PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09  
 PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11  
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
 NUMBER OF SEQ ID NOS: 115  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 56  
 LENGTH: 146  
 TYPE: PRT  
 ORGANISM: mus musculus  
 US-09-923-246-56  
 RESULT 14  
 Query Match 56.8%; Score 404; DB 2; Length 146;  
 Best Local Similarity 62.1%; Pred. No. 2e-38; e=63;  
 Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;  
 QY 2 QGDPRHRMIRMRQLIDIVDQKLVNDVPEFLPAPEDVETNEWSAFCFOAKLKSANT 61  
 Db 23 QGDPRHRMIRMRQLIDIVDQKLVNDVPEFLPAPEDVETNEWSAFCFOAKLKSANT 82  
 QY 62 GNNERIINVSIKKRKRPSTNAGRGRKRHRGKPCSDSYEKPPKEFLERFLQMH 121  
 Db 83 GNNKTFIDLVQQLRRLPARRGGKKQKHKIAKPCSDSYEKTPKEFLERFLQMH 142  
 QY 122 QHLS 125  
 Db 143 QHLS 146  
 RESULT 14  
 ; Sequence 56, Application US/10295723  
 ; Patent No. 6686178  
 GENERAL INFORMATION:  
 ; APPLICANT: No. 6686178ak, Julia E.  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Sprecher, Cindy A.  
 ; APPLICANT: Foster, Donald C.  
 ; APPLICANT: Holly, Richard D.  
 ; APPLICANT: Gross, Jane A.  
 ; APPLICANT: Johnston, Janet V.  
 ; APPLICANT: Nelson, Andrew J.  
 ; APPLICANT: Dillon, Stacey R.  
 ; APPLICANT: Hammond, Angela K.  
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND  
 FILE REFERENCE: 99-16  
 CURRENT APPLICATION NUMBER: US/10/295,723  
 CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: 09/522,217

PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: 1999-07-01  
; SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 56  
; LENGTH: 146

TYPE: PRT  
; ORGANISM: *mus musculus*  
US-10-295-723-56

Query Match 56.8%; Score 404; DB 2; Length 146;

Best Local Similarity 62.1%; Pred. No. 2e-38; Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 2 QGDPRHMRQLDIDVQDKNVDLVEFLPAPEDVETNEWSAFSCFOQAQLSANT 61  
Db 23 QGPDRLLRLRHLIDIVEQQLTYENDLDPPELISAPODVKGHCHEAAFCFOKAKLKPSNP 82

QY 62 GNNERIINVSIKKRKRPSTWAGRRQKHRLTCPSCSYKECPKELERFKSLQNMH 121  
Db 83 GNNKTFIDLVAGLRRLPARRGKQKHIACKCPSDOSYEKTRPKFELRKWLQNMH 142

QY 122 QHLS 125

Db 143 QHLS 146

RESULT 15  
US-09-825-561A-47

; Sequence 47, Application US/09825561A  
; Patent No. 6777539

GENERAL INFORMATION:

APPLICANT: Sorecher, Cindy A.  
; APPLICANT: No. 6777539ak, Julia E.

APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.

APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.

TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS  
FILE REFERENCE: 00-22

CURRENT APPLICATION NUMBER: US/09/825, 561A

PRIOR APPLICATION NUMBER: US 60/194, 731

PRIOR FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/222, 121

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 86

SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 47

; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: *Mus musculus*  
US-09-825-561A-47

Db 143 QHLS 146

Search completed: August 14, 2006, 21:53:20  
Job time : 49 secs

Query Match 56.8%; Score 404; DB 2; Length 146;  
; Best Local Similarity 62.1%; Pred. No. 2e-38; Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;  
; QY 2 QGDPRHMRQLDIDVQDKNVDLVEFLPAPEDVETNEWSAFSCFOQAQLSANT 61  
Db 23 QGPDRLLRLRHLIDIVEQQLTYENDLDPPELISAPODVKGHCHEAAFCFOKAKLKPSNP 82  
; QY 62 GNNERIINVSIKKRKRPSTWAGRRQKHRLTCPSCSYKECPKELERFKSLQNMH 121  
Db 83 GNNKTFIDLVAGLRRLPARRGKQKHIACKCPSDOSYEKTRPKFELRKWLQNMH 142

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OM protein - protein search, using sw model

Run on: August 14, 2006, 21:52:43 ; Search time 180 Seconds

Sequence: 1 MQGQDRHMRMQLDIVDQ...LLQKMIHQHSRRTGSEDS 134  
Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Title: Perfect score: 711  
Sequence: US-10-735-149-28

Total number of hits satisfying chosen parameters: 2097797  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : Listing first 45 summaries

Published Applications AA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US107\_PUBCOMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US10\_PUBCOMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US10B\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pupaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match Length | DB ID             | Description          |
|------------|-------|--------------------|-------------------|----------------------|
| 1          | 706   | 99.3               | 133               | 5 US-10-867-992-19   |
| 2          | 706   | 99.3               | 162               | 3 US-09-923-246-2    |
| 3          | 706   | 99.3               | 162               | 3 US-09-825-561A-10  |
| 4          | 706   | 99.3               | 162               | 3 US-09-922-218A-19  |
| 5          | 706   | 99.3               | 162               | 4 US-10-264-634-19   |
| 6          | 706   | 99.3               | 162               | 4 US-10-205-723-2    |
| 7          | 706   | 99.3               | 162               | 4 US-10-282-622-2    |
| 8          | 706   | 99.3               | 162               | 4 US-10-456-780-2    |
| 9          | 706   | 99.3               | 162               | 4 US-10-659-684-2    |
| 10         | 706   | 99.3               | 162               | 4 US-10-620-169-2    |
| 11         | 706   | 99.3               | 162               | 5 US-10-872-087-10   |
| 12         | 706   | 99.3               | 162               | 5 US-10-787-442-2    |
| 13         | 706   | 99.3               | 162               | 5 US-10-951-239-2    |
| 14         | 706   | 99.3               | 162               | 5 US-10-775-204-2177 |
| 15         | 706   | 99.3               | 162               | 6 US-11-174-398-2    |
| 16         | 706   | 99.3               | 162               | 6 US-11-134-489-2    |
| 17         | 706   | 99.3               | 162               | 6 US-11-132-947-9    |
| 18         | 706   | 99.3               | 162               | 6 US-11-197-488-19   |
| 19         | 706   | 99.3               | 174               | 5 US-10-775-204-2167 |
| 20         | 696   | 97.9               | 160               | 5 US-11-197-221-1    |
| 21         | 695   | 97.7               | 131               | 5 US-10-867-992-16   |
| 22         | 695   | 97.7               | 131               | 6 US-11-132-947-2    |
| 23         | 695   | 97.7               | 519               | 3 US-09-923-246-85   |
| 24         | 695   | 97.7               | 519               | 4 US-10-225-723-85   |
| 25         | 695   | 97.7               | 519               | 4 US-10-659-684-85   |
| 26         | 695   | 97.7               | 519               | 5 US-10-787-442-85   |
| 27         | 97.6  | 162                | 4 US-10-282-622-6 |                      |

#### ALIGNMENTS

RESULT 1  
US-10-867-992-19  
Query Match 99.3%; Score 706; DB 5; Length 133;  
Best Local Similarity 100.0%; Pred. No. 3.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 OSQGDRHMRMQLDIVDQKLNTVNDLJPEFLAPDVECTCEWSAFSCFPQKQLKSANT 61  
Db 1 QGQDRHMRMQLDIVDQKLNTVNDLJPEFLAPDVEDVETCEWSAFSCFPQKQLKSANT 60

QY 62 GNNERIINVKIKLKRKPSTNAGRQKRGRLCPSCSYKEKPKEELERPKSLQKMH 121  
Db 61 GNNERIINVKIKLKRKPSTNAGRQKRGRLCPSCSYKEKPKEELERPKSLQKMH 120

QY 122 OHSSRTGSEDS 134  
Db 121 OHSSRTGSEDS 133

RESULT 2  
US-09-923-246-2  
Sequence 2 Application US/09923246  
Patent No. US20020128446A1

GENERAL INFORMATION:

APPLICANT: NO. US20020128446A1

APPLICANT: presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.



PRIOR APPLICATION NUMBER: 60/373,746  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Human  
; US-10-264-634-19.

RESULT 6  
US-10-295-723-2  
; Sequence 2, Application US/10295723  
; Publication No. US20030125534A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20030125534A1  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Spracher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnson, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/10/295,723  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: 99/522,217  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,547  
; PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,904  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-295-723-2

Query Match 99.3%; Score 706; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QGODRHMIRMRQLIDIVDQLKNTVNDLVPFLPAPEDVETNCCEWSAFCFOQAQLKSANT 61  
Db 30 QGODRHMIRMRQLIDIVDQLKNTVNDLVPFLPAPEDVETNCCEWSAFCFOQAQLKSANT 89

RESULT 7  
US-10-282-622-2  
; Sequence 2, Application US/10282622  
; Publication No. US20030134390A1  
; GENERAL INFORMATION:  
; APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: No. US20030134390A1  
; TITLE OF INVENTION: ZALPHALL LIGAND ANTAGONISTS  
; FILE REFERENCE: 01-37  
; CURRENT APPLICATION NUMBER: US/10/282,622  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 60/337,586  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-282-622-2

Query Match 99.3%; Score 706; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QGODRHMIRMRQLIDIVDQLKNTVNDLVPFLPAPEDVETNCCEWSAFCFOQAQLKSANT 61  
Db 30 QGODRHMIRMRQLIDIVDQLKNTVNDLVPFLPAPEDVETNCCEWSAFCFOQAQLKSANT 89

RESULT 8  
US-10-456-780-2  
; Sequence 2, Application US/10456780  
; Publication No. US2004009150A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Hughes, Steven D.  
; APPLICANT: Holly, Richard D.  
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND  
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS  
; FILE REFERENCE: 03-08  
; CURRENT APPLICATION NUMBER: US/10/456,780  
; CURRENT FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/387,127  
; PRIOR FILING DATE: 2002-06-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-456-780-2

Query Match 99.3%; Score 706; DB 4; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QGODRHMIRMRQLIDIVDQLKNTVNDLVPFLPAPEDVETNCCEWSAFCFOQAQLKSANT 61  
Db 30 QGODRHMIRMRQLIDIVDQLKNTVNDLVPFLPAPEDVETNCCEWSAFCFOQAQLKSANT 89

30 QGDQDRHMIRMRQLIDIVDQKRNVNDLVFPIRPFEDVETNECSAFSCFOQAKLSANT 89  
 Db ; APPLICANT: Whitters, Matthew  
 Qy ; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH  
 62 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSCDSYEKPPKEFLRFKSLIQKMH 121  
 Db ; FILE REFERENCE: 22058-5B5  
 90 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSCDSYEKPPKEFLRFKSLIQKMH 149  
 Db ; CURRENT APPLICATION NUMBER: US/10/620,169  
 ; CURRENT FILING DATE: 2003-07-15  
 ; PRIOR APPLICATION NUMBER: 60/396,160  
 ; PRIOR FILING DATE: 2002-07-15  
 ; PRIOR APPLICATION NUMBER: 60/403,001  
 ; PRIOR FILING DATE: 2002-08-12  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SEQ ID NO: PatentIn Ver. 2.1  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

RESULT 9  
 US-10-659-684-2  
 ; Sequence 2, Application US/10659684  
 ; Publication No. US20040110932A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Specher, Cindy A.  
 ; APPLICANT: Foster, Donald C.  
 ; APPLICANT: Holly, Richard D.  
 ; APPLICANT: Gross, Jane A.  
 ; APPLICANT: Johnston, Janet V.  
 ; APPLICANT: Nelson, Andrew J.  
 ; APPLICANT: Dillon, Stacey R.  
 ; APPLICANT: Hammond, Angela K.  
 ; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND  
 ; FILE REFERENCE: 99-16  
 ; CURRENT APPLICATION NUMBER: US/10/659,684  
 ; CURRENT FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: US/09/522,217  
 ; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
 ; NUMBER OF SEQ ID NOS: 115  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-659-684-2

Query Match 99.3% Score 706; DB 4; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-67; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 100.0%;  
 ; Sequence 10, Application US/10872087  
 ; Publication No. US20040255743A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Specher, Cindy A.  
 ; APPLICANT: Novak, Julia E.  
 ; APPLICANT: West, James W.  
 ; APPLICANT: Holly, Richard D.  
 ; APPLICANT: Nelson, Andrew J.  
 ; TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS  
 ; FILE REFERENCE: 00-22D1  
 ; CURRENT APPLICATION NUMBER: US/10/872,087  
 ; CURRENT FILING DATE: 2004-06-18  
 ; PRIOR APPLICATION NUMBER: US 60/194,731  
 ; PRIOR FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/222,121  
 ; PRIOR FILING DATE: 2000-07-28  
 ; PRIOR APPLICATION NUMBER: US 09/825,561  
 ; PRIOR FILING DATE: 2001-04-03  
 ; NUMBER OF SEQ ID NOS: 85  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-872-087-10

Query Match 99.3% Score 706; DB 5; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-67; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 100.0%;  
 ; Sequence 12, Application US/10620169  
 ; Publication No. US20040136954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Grubbs, Michael J  
 ; APPLICANT: Wurster, Andrea  
 ; APPLICANT: Young, Deborah  
 ; APPLICANT: Collins, Mary

RESULT 12  
US-10-787-442-2  
; Sequence 2, Application US/10787442  
; Publication No. US20040260065A1  
; GENERAL INFORMATION:  
; APPLICANT: Novak, Julia E.  
; APPLICANT: presnell, Scott R.  
; APPLICANT: Spracher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI1 LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/10/787,442  
; CURRENT FILING DATE: 2004-02-26  
; PRIOR APPLICATION NUMBER: US/09/522,217  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,547  
; PRIOR FILING DATE: 1998-03-09  
; PRIOR APPLICATION NUMBER: US 60/123,904  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-787-442-2

Query Match 99.3%; Score 706; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 2  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-951-239-2

Query Match 99.3%; Score 706; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 2  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-951-239-2

RESULT 14  
US-10-775-204-2177  
; Sequence 2177, Application US/10775204  
; Publication No. US20050186664A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Balance, David J.  
; APPLICANT: Turner, Andrew J.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: P564  
; CURRENT APPLICATION NUMBER: US/10/775,204  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/341,811  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/360,000  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/378,950  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/398,008  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/411,355  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: 60/414,984  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/417,611  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/420,246  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: 60/423,623  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/351,360  
; PRIOR FILING DATE: 2002-01-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2222  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 2177  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-775-204-2177

Query Match 99.3%; Score 706; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
SEQ ID NO 2  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-775-204-2177

RESULT 13  
US-10-951-239-2  
; Sequence 2, Application US/10951239  
; Publication No. US20050095223A1  
; GENERAL INFORMATION:  
; APPLICANT: Sivakumar, Pallavar  
; APPLICANT: Nelson, Andrew  
; TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES  
; TITLE OF INVENTION: USING IL-21  
; FILE REFERENCE: 03-09  
; CURRENT APPLICATION NUMBER: US/10/951,239  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR APPLICATION NUMBER: 60/505,919  
; PRIOR FILING DATE: 2003-09-25

Db 30 QQQDRHIMRMRQLIDTVQDKNYVNDLVPEFLPAPEDVETNCWMSAFSCFQKAQLKSANT 89  
 Qy 62 GNNERIINVISSKKLKRKEPSTNAGRROKHLTCPSCSYKEKPKFELRFKSLQKMH 121  
 Db 90 GNNERIINVISSKKLKRKEPSTNAGRROKHLTCPSCSYKEKPKFELRFKSLQKMH 149  
 Qy 122 QHLSRTHGSEDS 134  
 Db 150 QHLSRTHGSEDS 162

RESULT 15  
 US-11-174-398-2

; Sequence 2, Application US/11174398  
 ; Publication No. US20050244930A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: West, James W.  
 ; APPLICANT: Novak, Julia E.  
 ; TITLE OF INVENTION: ZALPHAN LIGAND ANTAGONISTS  
 ; FILE REFERENCE: 01-37  
 ; CURRENT APPLICATION NUMBER: US/11/174,398  
 ; CURRENT FILING DATE: 2005-07-01  
 ; PRIOR APPLICATION NUMBER: US/10/282,622  
 ; PRIOR FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: 60/337,586  
 ; PRIOR FILING DATE: 2001-11-05  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-11-174-398-2

Query Match 99.3%; Score 706; DB 6; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QQQDRHIMRMRQLIDTVQDKNYVNDLVPEFLPAPEDVETNCWMSAFSCFQKAQLKSANT 61  
 Db 30 QQQDRHIMRMRQLIDTVQDKNYVNDLVPEFLPAPEDVETNCWMSAFSCFQKAQLKSANT 89  
 Qy 62 GNNERIINVISSKKLKRKEPSTNAGRROKHLTCPSCSYKEKPKFELRFKSLQKMH 121  
 Db 90 GNNERIINVISSKKLKRKEPSTNAGRROKHLTCPSCSYKEKPKFELRFKSLQKMH 149  
 Qy 122 QHLSRTHGSEDS 134  
 Db 150 QHLSRTHGSEDS 162

Search completed: August 14, 2006, 21:56:26  
 Job time : 180 secs

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GenCore version 5.1.9

Om protein - protein search, using sw model  
Run on: August 14, 2006, 21:53:33 ; Search time 33 Seconds  
Sequence: 1 MQGDRHMRQQLIDIVDQ.....LLQKMIHOHLSSRTHGSBDS 134  
Scoring table: BLOSUM62

Title: US-10-735-149-28  
Perfect score: 711  
Sequence: 1 MQGDRHMRQQLIDIVDQ.....LLQKMIHOHLSSRTHGSBDS 134  
Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SINS3/podata/1/pubpaas/us09\_NEW\_PUB.pep: \*  
2: /EMC\_Celerra\_SINS3/podata/1/pubpaas/us06\_NEW\_PUB.pep: \*  
3: /EMC\_Celerra\_SINS3/podata/1/pubpaas/us07\_NEW\_PUB.pep: \*  
4: /EMC\_Celerra\_SINS3/podata/1/pubpaas/us08\_NEW\_PUB.pep: \*  
5: /EMC\_Celerra\_SINS3/podata/1/pubpaas/PCT\_NEW\_PUB.pep: \*  
6: /EMC\_Celerra\_SINS3/podata/1/pubpaas/us10\_NEW\_PUB.pep: \*  
7: /EMC\_Celerra\_SINS3/podata/1/pubpaas/us11\_NEW\_PUB.pep: \*  
8: /EMC\_Celerra\_SIDS3/podata/1/pubpaas/us60\_NEW\_PUB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score or the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description          |
|------------|-------|--------------------|-------|----------------------|
| 1          | 711   | 100.0              | 134   | US-10-735-149-28     |
| 2          | 706   | 99.3               | 162   | US-10-511-937-2572   |
| 3          | 706   | 99.3               | 162   | US-10-735-149-2      |
| 4          | 706   | 99.3               | 162   | US-10-806-11-10      |
| 5          | 695   | 97.7               | 131   | US-10-806-611-2      |
| 6          | 524   | 73.7               | 122   | US-10-806-611-12     |
| 7          | 404   | 56.8               | 146   | US-10-806-611-13     |
| 8          | 394   | 55.4               | 122   | US-10-806-611-4      |
| 9          | 99.5  | 14.0               | 162   | US-10-511-937-2499   |
| 10         | 74.5  | 10.5               | 431   | US-11-056-355B-36356 |
| 11         | 74.5  | 10.5               | 431   | US-11-056-355B-45283 |
| 12         | 74.5  | 10.5               | 441   | US-11-056-355B-36355 |
| 13         | 74.5  | 10.5               | 441   | US-11-056-355B-45282 |
| 14         | 74.5  | 10.5               | 463   | US-11-056-355B-36354 |
| 15         | 74.5  | 10.5               | 463   | US-11-056-355B-45281 |
| 16         | 71    | 10.0               | 555   | US-11-056-355B-79971 |
| 17         | 71    | 10.0               | 631   | US-11-056-355B-79970 |
| 18         | 71    | 10.0               | 864   | US-11-056-355B-79969 |
| 19         | 70.5  | 9.9                | 352   | US-11-056-355B-81843 |
| 20         | 70.5  | 9.9                | 565   | US-10-471-571A-5038  |
| 21         | 70.5  | 9.8                | 861   | US-10-520-470-73     |
| 22         | 69.5  | 9.8                | 720   | US-10-449-902-51542  |
| 23         | 69.5  | 9.8                | 864   | US-11-251-208-77     |
| 24         | 69    | 9.7                | 707   | US-11-233-697-3241   |
| 25         | 68.5  | 9.6                | 212   | US-11-056-355B-4865  |

### ALIGNMENTS

| SEQ ID NO | LENGTH | TYPE: PRT         | ORGANISM: Artificial Sequence | FEATURE: OTHER INFORMATION: optimized IL-21 | US-10-735-149-28  |
|-----------|--------|-------------------|-------------------------------|---|---|
| 1         | 134    | Sequence 28, Appl | Sequence 2572, Ap             | Query Match                                 | 100.0%; Score 711; DB 6; Length 134;                          |
| 2         | 162    | Sequence 2, Appl  | Sequence 10, Appl             | Best Local Similarity                       | 100.0%; Score 711; DB 6; Length 134;                          |
| 3         | 162    | Sequence 2, Appl  | Sequence 12, Appl             | Matches                                     | 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;          |
| 4         | 162    | Sequence 13, Appl | Sequence 4, Appl              | Qy  | 1 MQGDRHMRQQLIDIVDQ.....LLQKMIHOHLSSRTHGSBDS 134              |
| 5         | 131    | Sequence 14, Appl | Sequence 36355, A             | Db  | 1 MQGDRHMRQQLIDIVDQ.....LLQKMIHOHLSSRTHGSBDS 134              |
| 6         | 122    | Sequence 15, Appl | Sequence 45282, A             | Qy  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 7         | 146    | Sequence 16, Appl | Sequence 45281, A             | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 8         | 122    | Sequence 17, Appl | Sequence 79971, A             | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 9         | 162    | Sequence 18, Appl | Sequence 79969, A             | Db  | 121 HOHLSSRTHGSBDS 134  |
| 10        | 162    | Sequence 19, Appl | Sequence 81843, A             | Qy  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 11        | 131    | Sequence 20, Appl | Sequence 5038, A              | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 12        | 122    | Sequence 21, Appl | Sequence 51542, A             | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 13        | 146    | Sequence 22, Appl | Sequence 77, A                | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 14        | 122    | Sequence 23, Appl | Sequence 3241, A              | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 15        | 162    | Sequence 24, Appl | Sequence 4865, A              | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 16        | 162    | Sequence 25, Appl |                               | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 17        | 131    | Sequence 26, Appl |                               | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 18        | 146    | Sequence 27, Appl |                               | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 19        | 122    | Sequence 28, Appl |                               | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 20        | 162    | Sequence 29, Appl |                               | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 21        | 162    | Sequence 30, Appl |                               | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 22        | 162    | Sequence 31, Appl |                               | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 23        | 162    | Sequence 32, Appl |                               | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |
| 24        | 162    | Sequence 33, Appl |                               | Qy  | 121 HOHLSSRTHGSBDS 134  |
| 25        | 162    | Sequence 34, Appl |                               | Db  | 61 TGNERNIINVSKKLRKPKPSNMGRQRKRUTCPSCDSYCKPPFLPERFKSLQKMI 120 |

### RESULT

### RESULT 2

### RESULT 3

### RESULT 4

### RESULT 5

### RESULT 6

### RESULT 7

### RESULT 8

### RESULT 9

### RESULT 10

### RESULT 11

### RESULT 12

### RESULT 13

### RESULT 14

### RESULT 15

### RESULT 16

### RESULT 17

### RESULT 18

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### RESULT 104

### RESULT 105

### RESULT 106

### RESULT 107

### RESULT 108

### RESULT 109

### RESULT 110

### RESULT 111

### RESULT 112

### RESULT 113

### RESULT 114

### RESULT 115

### RESULT 116

### RESULT 117

### RESULT 118

### RESULT 119

### RESULT 120

; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: F.Y. Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIORITY APPLICATION NUMBER: PCT/US2003/012946  
; PRIORITY FILING DATE: 2003-04-24  
; PRIORITY APPLICATION NUMBER: US 10/131,831  
; PRIORITY FILING DATE: 2002-04-24  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 2572  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-511-937-2572

Query Match 99.3%; Score 706; DB 6; Length 162;  
Best Local Similarity 100%; Pred. No. 1.1e-61; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 61  
Db 30 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 89

Qy 62 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 121  
Db 90 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 149

Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

RESULT 3  
; Sequence 2, Application US/10735149  
; Publication No. US20060134754A1  
; GENERAL INFORMATION:  
; APPLICANT: Chan, Chung  
; APPLICANT: Zamost, Bruce L.  
; APPLICANT: Covert, Douglas C.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: De Jongh, Karen S.  
; APPLICANT: Meyer, Jeffrey D.  
; APPLICANT: Holberman, Susan D.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21  
; FILE REFERENCE: 02-12  
; CURRENT APPLICATION NUMBER: US/10/735,149  
; CURRENT FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 2  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-735-149-2

Query Match 99.3%; Score 706; DB 6; Length 162;  
Best Local Similarity 100%; Pred. No. 1.1e-61; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 61  
Db 30 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 89

Qy 62 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 121  
Db 90 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 149

Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

RESULT 4  
; Sequence 10, Application US/10806611  
; Publication No. US20060159655A1  
; GENERAL INFORMATION:  
; APPLICANT: Collins, Mary  
; APPLICANT: Chin, Blaine Y.  
; APPLICANT: Senice, Mayra  
; APPLICANT: Young, Deborah A.  
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF  
; FILE REFERENCE: 16158-013001  
; CURRENT APPLICATION NUMBER: US/10/806,611  
; PRIORITY APPLICATION NUMBER: US 60/456,920  
; SEQ ID NO: 10  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-806-611-10

Query Match 99.3%; Score 706; DB 6; Length 162;  
Best Local Similarity 100%; Pred. No. 1.1e-61; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 61  
Db 30 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 89

Qy 62 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 121  
Db 90 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 149

Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

RESULT 5  
; Sequence 2, Application US/10806611  
; Publication No. US20060159655A1  
; GENERAL INFORMATION:  
; APPLICANT: Collins, Mary  
; APPLICANT: Chin, Blaine Y.  
; APPLICANT: Senice, Mayra  
; APPLICANT: Young, Deborah A.  
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF  
; FILE REFERENCE: 16158-013001  
; CURRENT APPLICATION NUMBER: US/10/806,611  
; CURRENT FILING DATE: 2004-03-22  
; PRIORITY APPLICATION NUMBER: US 60/456,920  
; SEQ ID NO: 13  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-806-611-2

Query Match 99.3%; Score 706; DB 6; Length 162;  
Best Local Similarity 100%; Pred. No. 1.1e-61; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 61  
Db 30 QGODRHMTRMQLIDIVDQLKVNLDVPEFLPAPEDVETNEWSAFSCFQKAQLSANT 89

Qy 62 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 121  
Db 90 GNNERIINVSIKKLKRKPSTNAGRRQKRHLTCPSDSYEKKPKPFLEFRFLQMIH 149

Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

; SEQ ID NO 2  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-806-611-2

Query Match 97.7%; Score 635; DB 6; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1e-60; Mismatches 0; Indels 0; Gaps 0;  
Matches 131; Conservative 0; ; N mismatches 0;

Qy 4 QDRHIMRQLDIDVQKVNVLVPEFLPAPEDDVETNCWNSAFSCFOKAQIKSANTGN 63  
Db 1 QDRHIMRQLDIDVQKVNVLVPEFLPAPEDDVETNCWNSAFSCFOKAQIKSANTGN 60

RESULT 6  
US-10-806-611-12  
Sequence 12, Application US/10806611  
Publication No. US20060159655A1

Qy 64 NERINVNSIKKLRKKPPSTNAGRQKRHLTCPSCSYEVKKPKFPLERFKSLIQQMTHQH 123  
Db 61 NERINVNSIKKLRKKPPSTNAGRQKRHLTCPSCSYEVKKPKFPLERFKSLIQQMTHQH 120

Qy 124 LSSTRHGSEDS 134  
Db 121 LSSTRHGSEDS 131

RESULT 7  
US-10-806-611-13  
Sequence 13, Application US/10806611  
Publication No. US20060159655A1

Qy 65 ERINIVNSIKKLRKKPPSTNAGRQKRHLTCPSCSYEVKKPKFPLERFKSLIQQMTHQH 124  
Db 62 KTFIIDLVAQRRLPARRGGSKQKHIAKCPSCSDSYEVKKPKFPLERFKSLIQQMTHQH 121

Qy 125 S 125  
Db 122 S 122

Query Match 56.8%; Score 404; DB 6; Length 146;  
Best Local Similarity 62.1%; Pred. No. 2.9e-32; Mismatches 77; Conservative 19; N mismatches 28; Indels 0; Gaps 0;  
Matches 146; ; N mismatches 28;

Qy 2 QGDPRHIMRQLDIDVQKVNVLVPEFLPAPEDDVETNCWNSAFSCFOKAQIKSANT 61  
Db 23 QGDPRHIMRQLDIDVQKVNVLVPEFLPAPEDDVETNCWNSAFSCFOKAQIKSANT 60

Qy 62 GNNERINVNSIKKLRKKPPSTNAGRQKRHLTCPSCSYEVKKPKFPLERFKSLIQQMTHQH 121  
Db 83 GNNKTFIDLAQDRLRRLPARRGGSKQKHIAKCPSCSDSYEVKKPKFPLERFKSLIQQMTHQH 142

Qy 122 OHHS 125  
Db 143 OHHS 146

RESULT 8  
US-10-806-611-4  
Sequence 4, Application US/10806611  
Publication No. US20060159655A1

GENERAL INFORMATION:  
; APPLICANT: Collins, Mary  
; APPLICANT: Chin, Blaine Y.  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 12  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; US-10-806-611-12

Query Match Best Local Similarity 80.3%; Score 524; DB 6; Length 122;  
Matches 98; Conservative 11; N mismatches 13; Indels 0; Gaps 0;  
; Software: Patentin version 3.2

Qy 4 QDRHIMRQLDIDVQKVNVLVPEFLPAPEDDVETNCWNSAFSCFOKAQIKSANTGN 63  
Db 1 QDRHIMRQLDIDVQKVNVLVPEFLPAPEDDVETNCWNSAFSCFOKAQIKSANTGN 60

RESULT 9  
US-10-806-611-4  
Sequence 4, Application US/10806611  
Publication No. US20060159655A1

GENERAL INFORMATION:  
; APPLICANT: Collins, Mary  
; APPLICANT: Chin, Blaine Y.  
; APPLICANT: Senices, Mayra  
; APPLICANT: Young, Deborah A.  
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF INTERLEUKIN-21 / INTERLEUKIN-21 RECEPTOR  
; CURRENT APPLICATION NUMBER: US/10/806,611  
; CURRENT FILING DATE: 2004-03-22  
; PRIOR APPLICATION NUMBER: 16158-013001  
; PRIOR FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 12  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; US-10-806-611-12

Query Match Best Local Similarity 80.3%; Score 524; DB 6; Length 122;  
Matches 98; Conservative 11; N mismatches 13; Indels 0; Gaps 0;  
; Software: Patentin version 3.2

Qy 64 NERINVNSIKKLRKKPPSTNAGRQKRHLTCPSCSYEVKKPKFPLERFKSLIQQMTHQH 123  
Db 61 NEKININITLKOLKRKLPATNTGRRQKRHTCPSCSYEVKKPKFPLERFKSLIQQMTHQH 120

Qy 124 LS 125  
Db 121 LS 122

RESULT 7  
US-10-806-611-13  
Sequence 13, Application US/10806611  
Publication No. US20060159655A1

GENERAL INFORMATION:  
; APPLICANT: Collins, Mary  
; APPLICANT: Chin, Blaine Y.  
; APPLICANT: Senices, Mayra  
; APPLICANT: Young, Deborah A.



Query Match 10.5%; Score 74.5; DB 7; Length 441;  
Best Local Similarity 21.8%; Pred. No. 15; Matches 26; Conservatve 24; Mismatches 48; Indels 21; Gaps 4;

Qy 6 REMIRMRQLIDIVDQLKQVNDLVPFLPAPEDVETNECSAFCQKAQLKSANTGNNE 65  
Db 230 KYKLAARKEFLDYNPELGNSYEVIT---APQDIATGGCALASFDRESLK----Q 277

Qy 66 RII-NVSIKKLKRKPSTNAGRQRKHRLTCPSCDSYEKKPKPKEPLERFKSLIQQMNHQ 123  
Db 278 KVIDNINFRNFLBLVLPDVRELINDPYSSRYASC-----LEYLASLKSNNLDIH 328

RESULT 13

US-11-056-355B-45282

; Sequence 45282, Application US/11056355B  
; Publication No. US20060150283A1

; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2/50-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056, 355B

; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544, 190

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 45282

; LENGTH: 441

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE: peptide

; LOCATION: (11):(41)

; OTHER INFORMATION: Ceres Seq. ID no. 13575997

; US-11-056-355B-45282

; Query Match 10.5%; Score 74.5; DB 7; Length 441;

; Best Local Similarity 21.8%; Pred. No. 15; Mismatches 26; Conservatve 24; Indels 21; Gaps 4;

; Matches 26; Conservatve 24; Mismatches 48; Indels 21; Gaps 4;

; TITLE OF INVENTION: Polypeptides Encoded Thereby

; FILE REFERENCE: 2/50-1590PUS2

; CURRENT APPLICATION NUMBER: US/11/056, 355B

; CURRENT FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544, 190

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 45281

; LENGTH: 463

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE: peptide

; LOCATION: (11):(43)

; OTHER INFORMATION: Ceres Seq. ID no. 13575996

; US-11-056-355B-45281

; Query Match 10.5%; Score 74.5; DB 7; Length 463;

; Best Local Similarity 21.8%; Pred. No. 16; Matches 26; Conservatve 24; Mismatches 48; Indels 21; Gaps 4;

; Matches 26; Conservatve 24; Mismatches 48; Indels 21; Gaps 4;

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2/50-1590PUS2

; CURRENT APPLICATION NUMBER: US/11/056, 355B

; CURRENT FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544, 190

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 36354

; LENGTH: 463

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE: peptide

; LOCATION: (11):(463)

; OTHER INFORMATION: Ceres Seq. ID no. 13575996  
; US-11-056-355B-36354

Query Match 10.5%; Score 74.5; DB 7; Length 463;  
Best Local Similarity 21.8%; Pred. No. 16; Matches 26; Conservatve 24; Mismatches 48; Indels 21; Gaps 4;

Qy 6 REMIRMRQLIDIVDQLKQVNDLVPFLPAPEDVETNECSAFCQKAQLKSANTGNNE 65  
Db 252 KYKLAARKEFLDYNPELGNSYEVIT---APQDIATGGCALASFDRESLK----Q 299

Qy 66 RII-NVSIKKLKRKPSTNAGRQRKHRLTCPSCDSYEKKPKPKEPLERFKSLIQQMNHQ 123  
Db 278 KVIDNINFRNFLBLVLPDVRELINDPYSSRYASC-----LEYLASLKSNNLDIH 328

RESULT 14

US-11-056-355B-36354

; Sequence 36354, Application US/11056355B

; Publication No. US20060150283A1

; GENERAL INFORMATION:

; APPLICANT: Brover, Vyacheslav

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

; FILE REFERENCE: 2/50-1590PUS2

; CURRENT APPLICATION NUMBER: US/11/056, 355B

; CURRENT FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544, 190

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 36354

; LENGTH: 463

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE: peptide

; LOCATION: (11):(463)

; OTHER INFORMATION: Ceres Seq. ID no. 13575996

; US-11-056-36354

; Query Match 10.5%; Score 74.5; DB 7; Length 463;

; Best Local Similarity 21.8%; Pred. No. 15; Matches 26; Conservatve 24; Mismatches 48; Indels 21; Gaps 4;

; Matches 26; Conservatve 24; Mismatches 48; Indels 21; Gaps 4;

; TITLE OF INVENTION: Polypeptides Encoded Thereby

; FILE REFERENCE: 2/50-1590PUS2

; CURRENT APPLICATION NUMBER: US/11/056, 355B

; CURRENT FILING DATE: 2005-02-14

; PRIOR APPLICATION NUMBER: 60/544, 190

; NUMBER OF SEQ ID NOS: 119966

; SEQ ID NO 36354

; LENGTH: 463

; TYPE: prt

; ORGANISM: Arabidopsis thaliana

; FEATURE: peptide

; LOCATION: (11):(463)

; OTHER INFORMATION: Ceres Seq. ID no. 13575996  
; US-11-056-36354

Search completed: August 14, 2006, 21:57:05  
Job time : 34 sec(s)

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Gencore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 14, 2006, 21:42:58 ; Search time 195 Seconds  
 (without alignments)  
 314.190 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711  
 Sequence: 1 MQGQDRHMINMRQLIDIVDQ.....LLQKMTIHOHLSRTHGSEDS 134

Scoring table: BIOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 437216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_ Geneseq 8:\*

- 1: geneseq1980s:\*
- 2: geneseq1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003s:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

| Result No. | Score | Query | Match Length | DB | ID        | Description                         |
|------------|-------|-------|--------------|----|-----------|-------------------------------------|
| 1          | 711   | 100.0 | 134          | 8  | ADP70485  | ADP70485 standard; protein; 134 AA. |
| 2          | 706   | 99.3  | 133          | 9  | ADW43687  | ADW43687 Mature hu                  |
| 3          | 706   | 99.3  | 162          | 3  | AAB18623  | Aab18623 A human z                  |
| 4          | 706   | 99.3  | 162          | 5  | AAB13729  | Aab13729 Human soil                 |
| 5          | 706   | 99.3  | 162          | 5  | AAU11965  | Aau11965 Human zal                  |
| 6          | 706   | 99.3  | 162          | 6  | ABR61407  | Abi61407 Human IL-                  |
| 7          | 706   | 99.3  | 162          | 7  | AAB14932  | Aab14932 Human int                  |
| 8          | 706   | 99.3  | 162          | 7  | ABD62893  | Abu62893 Human int                  |
| 9          | 706   | 99.3  | 162          | 7  | ADB85808  | Adb85808 Human int                  |
| 10         | 706   | 99.3  | 162          | 7  | ADP17046  | Adp17046 Human alb                  |
| 11         | 706   | 99.3  | 162          | 7  | ADP14572  | Adp14572 Human zal                  |
| 12         | 706   | 99.3  | 162          | 7  | ADP100908 | Adp100908 Immunity-                 |
| 13         | 706   | 99.3  | 162          | 8  | ADH10501  | Adh10501 Human int                  |
| 14         | 706   | 99.3  | 162          | 8  | ADJ25621  | Adj25621 Human int                  |
| 15         | 706   | 99.3  | 162          | 8  | ADM41017  | Adm41017 Human IL-                  |
| 16         | 706   | 99.3  | 162          | 8  | ADP12563  | Adp12563 Protein e                  |
| 17         | 706   | 99.3  | 162          | 7  | ADP19731  | Adp19731 Human zal                  |
| 18         | 706   | 99.3  | 162          | 8  | ADP70459  | Adp70459 Human int                  |
| 19         | 706   | 99.3  | 162          | 8  | ADB19031  | Adb19031 Full leng                  |
| 20         | 706   | 99.3  | 162          | 9  | ADW96355  | Adw96355 Human zal                  |
| 21         | 706   | 99.3  | 162          | 9  | ADY20419  | Ady20419 PRO polyp                  |
| 22         | 706   | 99.3  | 162          | 9  | ADY17792  | Ady17792                            |
| 23         | 706   | 99.3  | 162          | 9  | ADZ20501  | Adz20501 Human int                  |

#### ALIGNMENTS

RESULT 1  
 ADP70485  
 ID XX  
 AC ADP70485;  
 DT 23-SEP-2004 (first entry)  
 DE Codon optimised interleukin 21 (IL-21) protein SEQ ID NO:28.  
 KK interleukin 21; IL-21; human; codon optimised.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2004055168-A2.  
 XX  
 PD 01-JUL-2004.  
 XX  
 PF 12-DBC-2003; 2003WO-US039764.  
 PR 13-DEC-2002; 2002US-0433448P.  
 PR 13-DEC-2002; 2002US-0433452P.  
 PR XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Chang C, Zamost BL, Covert DC, Liu HY, De Jongh KS, Meyer JD;  
 PI Holderman SD;  
 XX  
 DR WPI; 2004-500211/47.  
 N-PSDB; ADP0484.

PT New expression vectors for the large-scale production of IL-21 proteins comprises a prokaryotic origin of replication, a transcriptional initiation DNA element, a polynucleotide sequence and a transcriptional terminator.

PS Claim 13; SEQ ID NO 28; 90pp; English.

XX

The present invention describes an expression vector for producing interleukin 21 (IL-21) protein. The expression vector comprises the following operably linked elements: (a) a prokaryotic origin of replication; (b) a transcriptional initiation DNA element; (c) an IL-21 polynucleotide sequence having the 405 base pair sequence given in SEQ ID NO:27 (ADP0484); and (d) a transcriptional terminator. Also described:

(1) a prokaryotic host cell transformed with the expression vector

XX

Aeb26428 Human int  
 Aed8671 Human int  
 Ael19679 Human int  
 Ag905273 Human IL-  
 Adt17042 Human alb  
 Aes52828 Human int  
 Adt69023 Mature hu  
 Adw43684 Predicted  
 Ael19672 Mature hu  
 Aab8627 Amino aci  
 Aau11971 MBP-human  
 Adt44655 Human Zal  
 Adt00991 MBP (malt  
 Adt19814 Human zal  
 Adw96438 Human zal  
 Ase14934 Human int  
 Adt2749 Human int  
 Adw43680 Human int  
 Adw43582 Human int  
 Adw43678 Human int  
 Adw43674 Human int  
 Adw43672 Human int

CC described above; (2) producing IL-21 proteins; (3) isolating insoluble IL  
 CC -21 protein, and (4) a composition comprising an IL-21 protein comprising  
 CC amino acids residues of the 134 amino acid sequence given in SEQ ID NO:28  
 CC (*ADP70485*) at a concentration of about 10 mg/ml IL-21 protein in 10 mM  
 CC histidine, and 4.7 % mannitol at pH 5.3. The composition and methods are  
 CC useful for the large-scale production of IL-21 in prokaryotic hosts. The  
 CC present sequence represents a human IL-21 protein which has been codon  
 CC optimised for prokaryotic expression, which is used in an example from  
 CC the present invention.

SQ Sequence 134 AA;

Query Match 100.0%; Score 711; DB 8; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 1.e-73; Mismatches 0; Indels 0; Gaps 0;  
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQODRMRMQLIDIVDQLKVNNDLVPEELPAPEDVETCWSAASCRCQAKQLSAN 60  
 Db 1 MQODRMRMQLIDIVDQLKVNNDLVPEELPAPEDVETCWSAASCRCQAKQLSAN 60

QY 61 TGNERNITINVKIKLKRKRPSTNAGRRQRKHLTCPSCDSYEKKPKPFLERKSLQKMI 120  
 Db 61 TGNERNITINVKIKLKRKRPSTNAGRRQRKHLTCPSCDSYEKKPKPFLERKSLQKMI 120

QY 121 HQHSSRTGSEDS 134  
 Db 121 HQHSSRTGSEDS 134

RESULT 2

ID ADW43687 standard; protein; 133 AA.  
 XX  
 AC ADW43687;  
 XX  
 DT 24-MAR-2005 (first entry)

DE Mature human interleukin-21.  
 XX  
 KW Interleukin-21; Antiallergic; Antiasthmatic; Antiparasitic;  
 KW Antiflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;  
 KW immune disorder; asthma; parasitic infection; inflammation;  
 KW multiple sclerosis; cancer; neoplasm; infection.  
 OS Homo sapiens.  
 XX  
 PN WO2004112703-A2.

XX  
 PD 29-DEC-2004.

XX  
 PF 15-JUN-2004; 2004WO-US018903.

PR 19-JUN-2003; 2003US-0479772P.

PA (CENZ ) CENTOCOR INC.

XX  
 PI Cunningham MR, Heavner GA, Luo J, Song XR;  
 XX  
 DR WPI; 2005-048751/05.

DR N-PSDB; ADW43686.

PT New poly nucleotides encoding interleukin-21 analogs, useful for treating  
 PT allergic diseases as well as asthma, parasitic diseases, inflammatory  
 PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.  
 XX  
 PS Claim 4; SEQ ID NO 19; 28pp; English.

The invention relates to an isolated poly nucleotides encoding interleukin  
 CC -21 analogs. Also included are the interleukin-21 analog proteins, a  
 vector comprising the poly nucleotide, an isolated host cell comprising  
 the vector and a process for producing a polypeptide comprising culturing  
 the host cell under conditions for production of the polypeptide. The  
 CC poly nucleotides and polypeptides, composition and method are useful for

CC treating allergic diseases as well as asthma, parasitic diseases,  
 CC inflammatory diseases such as multiple sclerosis, cancer, or infectious  
 CC diseases. The present sequence represents the wild-type mature human IL-  
 CC 21.  

SQ Sequence 133 AA;

Query Match 99.3%; Score 706; DB 9; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 4e-73; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRMRMQLIDIVDQLKVNNDLVPEELPAPEDVETCWSAASCRCQAKQLSANT 61  
 Db 1 QGODRMRMQLIDIVDQLKVNNDLVPEELPAPEDVETCWSAASCRCQAKQLSANT 60

QY 62 GNNERITINVKIKLKRKRPSTNAGRRQRKHLTCPSCDSYEKKPKPFLERKSLQKMI 121  
 Db 61 GNNERITINVKIKLKRKRPSTNAGRRQRKHLTCPSCDSYEKKPKPFLERKSLQKMI 120

QY 122 QHLSRTGSEDS 134  
 Db 121 QHLSRTGSEDS 133

RESULT 3

AAB18623  
 ID AAB18623 standard; protein; 162 AA.  
 XX  
 AC AAB18623;  
 XX  
 DT 22-JAN-2001 (first entry)

XX  
 DE A human zalphall ligand polypeptide.  
 XX  
 KW zalphall ligand; cytokine; hematopoietic cell proliferation; lymphoma;  
 KW tumourigenesis; leukemia; hematopoiesis; B cell tumour.  
 OS Homo sapiens.  
 XX  
 PN WO200053761-A2.

XX  
 PD 14-SEP-2000.

XX  
 PF 09-MAR-2000; 2000WO-US006067.

XX  
 PR 09-MAR-1999; 99US-00264908.

PR 11-MAR-1999; 99US-00265992.

PR 01-JUL-1999; 99US-0142013P.

XX  
 PA (ZYMO ) ZYMOGENETICS INC.

XX  
 PT Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;  
 PT Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
 XX  
 DR WPI; 2000-565600/52.  
 DR N-PSDB; AAN7552.

XX  
 PT New human cytokine, designated zalphall ligand, useful for stimulating  
 PT the proliferation and/or development of hematopoietic cells in vitro and  
 PT in vivo, and for treating tumorigenesis.

XX  
 PS Disclosure; Page 205-206; 256pp; English.

The present sequence represents a human zalphall ligand polypeptide,  
 CC which is a cytokine. The zalphall ligand is useful for stimulating the  
 proliferation and development of haematopoietic cells in vitro and in  
 vivo. Zalphall ligand poly nucleotides can be used as primers or probes  
 CC for cloning the zalphall gene. The zalphall ligand is useful for treating  
 CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for  
 CC treating leukaemia and lymphomas. Antagonists against zalphall ligand  
 CC are useful as research reagents for characterizing ligand-receptor  
 CC interaction. Antagonists are also useful for inhibiting expansion,  
 CC proliferation, activation and differentiation of cells involved in

CC regulating hematopoiesis. The zalphall ligand may also be used to  
 CC stimulate an immune response against B cell tumour, a virus, a parasite  
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,  
 CC agonists and antibodies are also useful for the detection, diagnosis,  
 CC prevention, and treatment of diseases associated with a zalphall ligand  
 CC genetic defect.

XX Sequence 162 AA;

Query Match 99.3%; Score 705; DB 3; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-73; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 0; PT PS SQ  
 OQGDQHMRMQLDIVDOLKNVNDLVEFLPAPEDVETNCWSAFSCPKQAKLSANT 61  
 QGDQHMRMQLDIVDOLKNVNDLVEFLPAPEDVETNCWSAFSCPKQAKLSANT 89  
 62 GNNERITINVSKKLRKRPSTNAGRQKRHLTCPSCDSYEKKPKFELRFKSLLQKMH 121  
 90 GNNERITINVSKKLRKRPSTNAGRQKRHLTCPSCDSYEKKPKFELRFKSLLQKMH 149  
 122 QHSSRTGSEDS 134  
 150 QHSSRTGSEDS 162

RESULT 4

XX AAE13729  
 ID AAE13729 standard; protein; 162 AA.XX AAE13729;  
 AC  
 XX DT 26-FEB-2002 (first entry)

XX Human soluble Zalphall cytokine receptor ligand protein.

KW Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;  
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW myasthenia gravis; systemic lupus erythematosus (SLE); diabetes;  
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease;  
 KW viral infection (dengue virus infection) and cancer. The present  
 OS sequence is human soluble Zalphall cytokine receptor ligand

OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Peptide 1..31 /label= Signal\_Peptide  
 FT Protein 32..162 /label= Mature\_Zalphall\_ligand  
 FT Region 41..56 /label= Helix\_A  
 FT Region 69..84 /label= Helix\_B  
 FT Region 92..105 /label= Helix\_C  
 FT Region 135..148 /label= Helix\_D  
 FT Region 136..138 /note= "Conserved region"

RESULT 5

XX AAU11965  
 ID AAU11965 standard; protein; 162 AA.XX AAU11965;  
 AC  
 XX DT 09-APR-2002 (first entry)

XX Human zalphall Ligand polypeptide.

KW Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;  
 KW natural killer cell proliferation; T-cell proliferation;  
 KW B-cell proliferation; anti-tumour; immune system;  
 KW immunomodulant; cytotoxic; human; hBcS;  
 KW activated human peripheral blood cell.

OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Peptide 1..31 /label= Signal\_Peptide  
 FT Protein 32..162 /label= Mature\_Zalphall\_ligand  
 PR 03-APR-2001; 2001WO-US010872.  
 XX 05-APR-2000; 2000US-0194731P.  
 PR 28-JUL-2000; 2000US-0222121P.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

XX WPI: 2002-025898/03.  
 DR N-PSDB; AAD22923.

PT Novel soluble receptor polypeptides and polynucleotides used as cytokine  
 PT antagonist for stimulating ligand activity-induced proliferation of  
 PT hematopoietic cells and for suppressing immune response in a mammal.

XX Sequence 162 AA;

Query Match 99.3%; Score 706; DB 5; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-73; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 0; PT PS SQ  
 OQGDQHMRMQLDIVDOLKNVNDLVEFLPAPEDVETNCWSAFSCPKQAKLSANT 61  
 QGDQHMRMQLDIVDOLKNVNDLVEFLPAPEDVETNCWSAFSCPKQAKLSANT 89  
 62 GNNERITINVSKKLRKRPSTNAGRQKRHLTCPSCDSYEKKPKFELRFKSLLQKMH 121  
 90 GNNERITINVSKKLRKRPSTNAGRQKRHLTCPSCDSYEKKPKFELRFKSLLQKMH 149  
 122 QHSSRTGSEDS 134  
 150 QHSSRTGSEDS 162

RESULT 5

XX AAU11965  
 ID AAU11965 standard; protein; 162 AA.XX AAU11965;  
 AC  
 XX DT 09-APR-2002 (first entry)

XX Human zalphall Ligand polypeptide.

KW Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;  
 KW natural killer cell proliferation; T-cell proliferation;  
 KW B-cell proliferation; anti-tumour; immune system;  
 KW immunomodulant; cytotoxic; human; hBcS;  
 KW activated human peripheral blood cell.

OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Peptide 1..31 /label= Signal\_Peptide  
 FT Protein 32..162 /label= Mature\_Zalphall\_ligand  
 PR US6307024-B1.  
 XX 23-OCT-2001.  
 PD 09-MAR-2000; 2000US-00522217.

|    |                                     |   |                |
|----|-------------------------------------|---|----------------|
| XX | PR                                  | 09-MAR-1999;  | 99US-0123547P. |
| XX | PR                                  | 11-MAR-1999;  | 99US-0123904P. |
| XX | PR                                  | 01-JUL-1999;  | 99US-0142013P. |
| XX | PA                                  | (ZYMO ) ZYMOGENETICS INC.   |                |
| XX | PI                                  | Novak JB, Preussnall SR, Sprecher CA, Foster DC, Holly RD;  |                |
| XX | PI                                  | Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  |                |
| XX | DR                                  | WPI; 2002-040208-05.  |                |
| XX | N-PSDB;                             | AAS20637.   |                |
| XX | PT                                  | New zalphall ligand polypeptides and poly nucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an antigenic response.   |                |
| XX | PT                                  |   |                |
| XX | PS                                  | Claim 7; Col 125-126; 105pp; English.   |                |
| XX | SQ                                  | Sequence 162 AA;  |                |
| XX | RESULT 6                            |   |                |
| ID | ABR61407                            | Query Match Best Local Similarity 99.3%; Score 706; DB 5; Length 162;   |                |
| AC | ABR61407 standard; protein; 162 AA. | Matches 133; Conservative 0; Mis matches 0; Delels 0; Gaps 0  |                |
| DT | 12-AUG-2003 (first entry)           |   |                |
| DE | Human IL-21 SEQ ID NO:19.           |   |                |
| XX | KW                                  | arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R; immune cell activity; cancer; infectious disorder; antirheumatic; antiarthritic; osteopathic; antiperiorotic; antirheumatic; antibacterial; viricide; antiparasitic; immunosuppressive; antidiabetic; dermatological; neuroprotective; antiulcer; antiallergic; antiangiogenic; hepatoprotective; antithyroid; antiinflammatory; immune response; immune disorder; |                |

XX OS autoimmune disease; human.  
 XX OS  
 XX PN  
 XX WO2003028630-A2.  
 XX PD 10-APR-2003.  
 XX PR 04-OCT-2002; 2002WO-US029839.  
 XX PR 04-OCT-2001; 2001US-00972218.  
 XX PR 17-APR-2002; 2002US-0373746P.  
 XX PA (AMHMP ) WYETH.  
 XX Carter L, Whitters MJ, Collins M, Young DA, Larsen G, Ma M, Wittek JS, Kasai MT;  
 PI Donaldson DD, Lowe LD, Dunnick K, Ma M;  
 PI Unger M;  
 DR WPI; 2003-430146/40.  
 DR N-PADB; ACC80873.  
 XX PT Treating or preventing arthritic disorder, cancer or infectious disorders  
 PT in a subject, involves administering a modulator of interleukin-21 or its  
 PT receptor which modulate immune cell activity.  
 XX Disclosure; Page 37; 17app; English.  
 CC The invention relates to a novel method for treating or preventing an  
 CC arthritic disorder in a subject. The method involves administering to the  
 CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist  
 CC optionally in combination with another therapeutic agent, to inhibit or  
 CC treat immune cell activity in the subject. The method is also useful for  
 CC treating or preventing cancer or an infectious disorder, in a subject, by  
 CC administering IL-21/IL-21R agonist, to increase immune cell activity. The  
 CC method of the invention has antirheumatic, antiarthritic, osteopathic,  
 CC antipsoriatic, cytostatic, antibacterial, viricide, antiparasitic,  
 CC immunosuppressive, antidiabetic, neuroprotective, dermatological,  
 CC antitulcer, antiasthmatic, antiallergic, antianaemic, hepatotropic,  
 CC antithyroid, and antiinflammatory activity. The method is useful for  
 CC treating or preventing an arthritic disorder such as rheumatoid  
 CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic  
 CC arthritis or ankylosing spondylitis, and also cancer such as solid  
 CC tumour, soft tissue tumour or metastatic lesion, or an infectious  
 CC disorder such a bacterial, viral or parasitic infection in a mammal,  
 CC preferably human. A method of the invention is also is useful for  
 CC increasing the ability of a vaccine composition containing an antigen to  
 CC elicit a protective immune response in a subject against the antigens.  
 CC The antigen is from a pathogen such as virus, bacterium or protozoan, or  
 CC from cancer or tumour cell antigen, or expressed on the surface of cancer  
 CC cell. An alternative method of the invention is useful for modulating the  
 CC activity of immune or hematopoietic cells and thus to treat or prevent a  
 CC variety of immune disorders, such as autoimmune diseases, for example  
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus  
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,  
 CC hepatitis, Graves' disease, graft versus host disease, and scleroderma.  
 CC The present sequence is used in an exemplification of the invention  
 Sequence 162 AA;

Db 150 QHLSRTHGSEDS 162  
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
 CC myasthenia gravis and diabetes. The polypeptides can also be used to  
 CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,  
 CC and for enhancing in vivo killing of target tissues. The present sequence  
 CC is human IL-21 (originally designated zalpha1II ligand)  
 XX SQ Sequence 162 AA;  
 XX Human interleukin-21 (IL-21).  
 XX Result 7  
 XX ID AAB14932 standard; protein; 162 AA.  
 XX AC AAB14932;  
 XX DT 27-AUG-2003 (first entry)  
 XX DE Human interleukin-21 (IL-21).  
 XX KW Interleukin-21; IL-21; antagonist; cancer; inflammatory;  
 XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis;  
 XX systemic lupus erythematosus; myasthenia gravis; diabetes; human;  
 XX zalpha1II ligand.  
 XX OS Homo sapiens.  
 XX FH location/Qualifiers  
 XX FT Region 41..55 /label= Helix\_A  
 XX FT Binding-site 44 /note= "Important for IL-21 binding to its receptor"  
 XX FT /note= "Important for IL-21 binding to its receptor"  
 XX FT Region 47 .68 /label= B/C\_loop  
 XX FT Region 57..68 /label= A/B\_loop  
 XX FT Region 69..84 /label= Helix\_B  
 XX FT Region 85..91 /label= B/C\_loop  
 XX FT Region 92..105 /label= Helix\_C  
 XX FT Region 106..134 /label= C/D\_loop  
 XX FT Region 135..148 /label= Helix\_D  
 XX FT Binding-site 135 /note= "Important for IL-21 binding to its receptor"  
 XX PN WO2003040313-A2.  
 XX PD 15-MAY-2003.  
 XX PR 28-OCT-2002; 2002WO-US034502.  
 XX PR 05-NOV-2001; 2001US-0337586P.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Presnell SR, West JW, Novak JB;  
 XX DR WPI; 2003-441547/41.  
 XX DR -PSDB; AAD47852.  
 XX PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing  
 PT and treating disorders with aberrant expression or activity of the IL-21  
 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and  
 PT diabetes.  
 PS Disclosure; Page 53-54; 71pp; English.  
 XX The invention relates to polynucleotides and polypeptides of interleukin-  
 CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50  
 CC that is not detectable in receptor binding studies. The antagonists of  
 CC the invention have mutations in the D helix of the IL-21 molecule, and  
 CC can be used to inhibit the activity of IL-21 with its cognate receptor.  
 CC The IL-21 antagonists are useful for diagnosing and treating disorders  
 CC involving the aberrant expression or activity of the IL-21 polypeptide,  
 CC such as cancer, inflammatory and autoimmune disorders, including

CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
 CC myasthenia gravis and diabetes. The polypeptides can also be used to  
 CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,  
 CC and for enhancing in vivo killing of target tissues. The present sequence  
 CC is human IL-21 (originally designated zalpha1II ligand)  
 XX SQ Sequence 162 AA;  
 XX Query Match 99.3%; Score 706; DB 7; Length 162;  
 XX Best Local Similarity 100.0%; Pred. No. 5 2e-73;  
 XX Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX AC ABU62893 standard; protein; 162 AA.  
 XX DT 15-SEP-2003 (first entry)  
 XX DB Human interleukin 21 (IL-21).  
 XX KK Human; MU-1; haemopoietin receptor superfamily chain; immunomodulator;  
 KK cyrostatic; antibacterial; virucide; antianaemic; gene therapy;  
 KK haematopoiesis; anaemias; immune response; cancer; infection;  
 KK transplanted organ; cytokine; receptor; interleukin 21; IL21.  
 XX OS Homo sapiens.  
 XX PN US2003049798-A1.  
 XX PD 13-MAR-2003.  
 XX PR 04-OCT-2001; 2001US-00972218.  
 XX PR 17-MAR-1998; 98US-00040005.  
 XX PR 28-APR-2000; 2000US-00560766.  
 XX PR 11-MAY-2000; 2000US-00569384.  
 XX PA (CART/) CARTER L.  
 XX PA (WHIT/) WHITTERS M J.  
 XX PA (COLL/) COLLINS M.  
 XX PA (YOUN/) YOUNG D A.  
 XX PA (DONA/) DONALDSON D D.  
 XX PA (LOWE/) LOWE L D.  
 XX PA (UNGER/) UNGER M.  
 XX PI Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;  
 XX PI Lowe LD, Unger M;  
 XX DR WPI; 2003-512354/48.  
 XX DR N-PSDB; ACD26729.  
 XX PT New fusion polypeptide for regulating hematopoiesis and immune responses,  
 PT comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion  
 PT polypeptide.  
 XX PS Disclosure; Page 10; 26pp; English.  
 XX CC The invention describes a fusion polypeptide comprising at least a

CC fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of CC anaemias) and/or immune responses (e.g. immune response to cancer, CC infections or to a transplanted organ) and in identifying other members CC of the haemopoietin superfamily, including cytokines and receptors. The CC polynucleotide may be used to express recombinant protein for analysis, CC characterisation or therapeutic use; and as markers for tissues or CC chromosomes. The polypeptide and polynucleotide may also be used as CC nutritional sources or supplements. This is the amino acid sequence of CC human interleukin 21 (IL21), a cytokine receptor that can be used to CC characterise the novel haemopoietin receptor of the invention.

XX Sequence 162 AA;

Query Match 99.3%; Score 706; DB 7; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGDPRHIMRMQLIDIVDQLKNVNDLVPEFLPAPEDVETNECEWSAFSCFOKAOLKSANT 61  
Db 30 QGDPRHIMRMQLIDIVDQLKNVNDLVPEFLPAPEDVETNECEWSAFSCFOKAOLKSANT 89

Qy 62 GNNERIINVSIKKLKRKPSTNAGRQRKHLTCPSCSYEKPPKEPLERFSLQMIH 121  
Db 90 GNNERIINVSIKKLKRKPSTNAGRQRKHLTCPSCSYEKPPKEPLERFSLQMIH 149

Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

RESULT 9  
ADE85808 ID ADE85808 standard; protein; 162 AA.

AC ADBE85808;  
XX DT 29-JAN-2004 (first entry)

DE Human interleukin-21.

KW Human; interleukin-21; immunosuppressive; antirheumatic; antiarthritic; KW antiinflammatory; dermatological; ophthalmological; uropathic; KW muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic; KW neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy.

OS Homo sapiens.

PN WO2003087320-A2.  
XX PD 23-OCT-2003.

PP 08-APR-2003; 2003WO-US010736.

XX PR 09-APR-2002; 2002US-0371038P.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

PT Moll T, Strom TB, Zheng XX;

XX DR WPI; 2003-845317/78.

PS Disclosure; SEQ ID NO 1; 65pp; English.

CC New substantially pure interleukin-21 polypeptide, useful for diagnosing, CC treating and prognosticating autoimmune disorders, e.g. rheumatic CC disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis CC and myasthenia gravis.

The present sequence is the protein sequence of human interleukin-21 (IL- CC 21). The invention provides antagonists of the IL-21 receptor. These CC include mutants of murine IL-21 in which the Gln residue at position 119 CC of the mature polypeptide is substituted by Asp or in which the Gln CC

residues at positions 114 and 119 of the mature polypeptide are both replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell activation. They preferably comprise a sequence that increases circulating half-life, such as the Fc region of an IgG molecule and may further comprise an antigenic tag. Such antagonists inhibit cellular proliferation in response to either anti-CD3 monoclonal antibodies or anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with IL-21. A claimed method of suppressing the immune response in a patient comprises administering the IL-21 antagonist or a nucleic acid encoding it. The method is used to treat an autoimmune disease such as rheumatic disease, including systemic lupus erythematosus, Sjogren's syndrome, scleroderma, mixed connective tissue disease, dermatomyositis, polymyositis, Reiter's syndrome, or Behet's disease, or rheumatoid arthritis, type I diabetes, autoimmune disease of the thyroid such as Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the central nervous system such as multiple sclerosis, myasthenia gravis, or encephalomyelitis, or an autoimmune disease selected from pemphigus vulgaris, pemphigus vegetans, pemphigus foliaceus, Sennar-Ulher syndrome, Brazilian pemphigus, psoriasis or inflammatory bowel disease (all claimed).

XX Sequence 162 AA;

Query Match 99.3%; Score 706; DB 7; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QGDPRHIMRMQLIDIVDQLKNVNDLVPEFLPAPEDVETNECEWSAFSCFOKAOLKSANT 61  
Db 30 QGDPRHIMRMQLIDIVDQLKNVNDLVPEFLPAPEDVETNECEWSAFSCFOKAOLKSANT 89

Qy 62 GNNERIINVSIKKLKRKPSTNAGRQRKHLTCPSCSYEKPPKEPLERFSLQMIH 121  
Db 90 GNNERIINVSIKKLKRKPSTNAGRQRKHLTCPSCSYEKPPKEPLERFSLQMIH 149

Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

RESULT 10  
ADP1746 ID ADP1746 standard; protein; 162 AA.

AC ADP1746;  
XX DT 12-FEB-2004 (first entry)

XX DB Human albumin fusion protein-related protein SeqIdn2177.

XX KW albumin fusion protein; albumin activity; human serum albumin; KW serum osmotic pressure; shelf-life; stability; antidiabetic; KW gene therapy; diabetes mellitus; human; gene; ds.

OS Homo sapiens.

PN WO2003060071-A2.

XX PD 24-JUL-2003.

XX PR 23-DEC-2002; 2002WO-US040891.

XX PR 21-DEC-2001; 2001US 0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US 0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-037022P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0383123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.  
 PR 24-JUL-2002; 2002US-0398008P.  
 PR 09-AUG-2002; 2002US-0402131P.  
 PR 13-AUG-2002; 2002US-0402708P.  
 PR 18-SEP-2002; 2002US-0411355P.  
 PR 02-OCT-2002; 2002US-0414984P.  
 PR 11-OCT-2002; 2002US-0417611P.  
 PR 23-OCT-2002; 2002US-0420246P.  
 PR 05-NOV-2002; 2002US-0423623P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (DELB-) DELTA BIOTECHNOLOGY LTD.  
 PA (PRIN-) PRINCIPIA PHARM CORP.  
 PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;  
 DR N-FSDB; ADF17040.  
 PT New albumin fusion protein, useful for preparing a composition for  
 PT treating diabetes mellitus.  
 XX  
 PS Example 4; SEQ ID NO 2177; 24pp; English.  
 CC This invention relates to a novel albumin fusion protein having albumin  
 CC or biological activity. Human serum albumin is responsible for a  
 CC significant proportion of the osmotic pressure of serum and also  
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of  
 CC albumin to a therapeutic protein may increase shelf-life and stability of  
 CC the therapeutic protein. The albumin fusion protein of the invention may  
 CC allow production or compositions with antidiabetic activity whilst the  
 CC nucleotide sequence which encodes it may be useful for gene therapy. The  
 CC albumin fusion protein is useful for preparing a composition for treating  
 CC diabetes mellitus. The present sequence is that of a therapeutic protein  
 CC which was fused with human albumin to create a novel albumin fusion  
 CC protein of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpat\_sequences  
 XX  
 SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 7; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-73; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 0;

QY 2 QGQDRHMTRMQLOIDIVQQLKNTVNDLVPEFLPAPEDVETNCWSAFCQKQLKSANT 61  
 Db 30 QGQDRHMTRMQLOIDIVQQLKNTVNDLVPEFLPAPEDVETNCWSAFCQKQLKSANT 89  
 Qy 62 GNNTERIINVISIKLKRPSTNAGRKRQHLTCSQSYKKPKEPLERFKSLQKMH 121  
 Db 90 GNNTERIINVISIKLKRPSTNAGRKRQHLTCSQSYKKPKEPLERFKSLQKMH 149  
 Qy 122 QHLSRSRTGSEDS 134  
 Db 150 QHLSRSRTGSEDS 162

RESULT 11  
 ADH4572  
 ID ADH4572 standard; protein; 162 AA.  
 DE Human Zalphall ligand protein.  
 XX  
 AC ADH4572;  
 DT 25-MAR-2004 (first entry)

Query Match 99.3%; Score 706; DB 7; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-73; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 0;

QY 2 QGQDRHMTRMQLOIDIVQQLKNTVNDLVPEFLPAPEDVETNCWSAFCQKQLKSANT 61  
 Do 30 QGQDRHMTRMQLOIDIVQQLKNTVNDLVPEFLPAPEDVETNCWSAFCQKQLKSANT 89

KW immunocompromised patient; HIV infection; vaccine; chromosome 4q27.  
 KW XX OS Homo sapiens.  
 KW XX  
 FH Key Peptide Location/Qualifiers  
 FT Protein 1..31 /note= "Signal peptide"  
 FT Protein 32..162 /note= "Mature Zalphall, claimed in claim 1n  
 XX US6605272-B2.  
 PN XX PD 12-AUG-2003.  
 XX PP 03-AUG-2001; 2001US-00923246.  
 XX PR 09-MAR-1999; 99US-0123547P.  
 PR 11-MAR-1999; 99US-0123908P.  
 PR 01-JUL-1999; 99US-0142013P.  
 PR 09-MAR-2000; 2000US-00522217.  
 XX PA (ZIMO ) ZYMOGENETICS INC.  
 XX PI Novak JE, Presnall SR, Sprecher CA, Foster DC, Holly RD;  
 PI Gross JA, Johnson JV, Nelson AJ, Dillon SR, Hammond AK;  
 DR XX WPI; 2003-895283/82.

PT Stimulating an immune response in a mammal exposed to an antigen or  
 PT tumor progression or metastasis, comprises administering zalphall ligand  
 PT polypeptide.  
 XX PS Claim 1; SEQ ID NO 2; 103pp; English.  
 CC The invention relates to stimulating an immune response in a mammal  
 CC exposed to an antigen or pathogen comprises administering a composition  
 CC comprising mature zalphall ligand polypeptide comprising residues 32-162  
 CC of ADH4572 in a pharmaceutical vehicle. Also included are stimulating an  
 CC immune response in a mammal exposed to an antigen or pathogen  
 CC (comprising: (a) determining (indirectly) the level of antigen or  
 CC pathogen present in the mammal; (b) administering a composition  
 CC comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)  
 CC determining (indirectly) the level of antigen or pathogen in the mammal;  
 CC and (d) comparing the antigen or pathogen level in (a) with (b), where a  
 CC change in the level indicates stimulation of immune response); and  
 CC simulating an immune response in a mammal exposed to an antigen or  
 CC pathogen (comprising: (a) determining a level of antigen- or pathogen-  
 CC specific antibody; (b) administering a composition comprising zalphall  
 CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post  
 CC administration level of the antigen- or pathogen-specific antibody; and  
 CC (d) comparing the level of the antibody in (a) with (b), where an  
 CC increase in the antibody level indicates stimulation of immune response).  
 CC The method is useful for stimulating an immune response in a mammal  
 CC exposed to an antigen or pathogen, and for enhancing anti-tumour activity  
 CC resulting in a reduction in tumour progression, decrease in metastasis,  
 CC or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma  
 CC or a B cell tumour. The zalphall ligand is useful for treating a wide  
 CC range of diseases arising from defects in the immune system, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or  
 CC diabetes, for boosting immunity to infectious diseases, treating  
 CC immunocompromised patients, such as HIV+ patients and in improving  
 CC vaccines. The present sequence is a human Zalphall ligand protein.  
 XX  
 SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 7; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-73; Mismatches 0; Indels 0; Gaps 0;  
 Matches 133; Conservative 0;



QY 122 QHLSRTGSEDS 134  
 ||||| ||||| |||||  
 Db 150 QHLSRTGSEDS 162

RESULT 14  
 ADJ25621; ID ADJ25621; standard; protein; 162 AA.  
 XX AC ADJ25621;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Human interleukin 21 (IL-21) protein SEQ ID NO:2.  
 XX KW interferon gamma inhibition; IFNgamma inhibition; interleukin 21 agonist; IL-21 agonist; antiasthmatic; antiallergic; antiarthritic; neuroprotective; antiinflammatory; dermatological; immuno suppressive; muscular; antipsoriatic; T helper; Th1; Th2; asthma; allergy; rheumatoid arthritis; multiple sclerosis; lupus; diabetes; Crohn's disease; psoriasis; myasthenia gravis; human; IL-21.  
 OS Homo sapiens.  
 XX PN WO2004007682-A2.  
 XX PD 22-JAN-2004.  
 XX PF 15-JUL-2003; 2003WO-US021975.  
 PR 15-JUL-2002; 2002US-0396160P.  
 PR 12-AUG-2002; 2002US-0403001P.  
 XX PA (AMHP ) WYETH.  
 PA (HARD ) HARVARD COLLEGE.  
 XX PI Grusby M, Wurster A, Young DA, Collins M, Whitter MJ;  
 XX DR WPI; 2004-122921/12.  
 DR N-PSDB; ADJ25620.  
 PT Inhibiting interferon gamma (IFNgamma) levels and T helper cell development and function in a T cell or cell population using IL-21 modulators, useful for the preventing and/or treating asthma, allergy, PT arthritis, lupus and diabetes.  
 XX RS Claim 1; SEQ ID NO 2; 59PP; English.  
 XX SQ sequence 162 AA;

The present invention describes a method for inhibiting interferon gamma (IFNgamma) levels in a T cell population by contacting the T cell or cell population with an interleukin 21 (IL-21) agonist in an amount sufficient to inhibit IFNgamma in the T cell or cell population, wherein the agonist is an IL-21 polypeptide comprising an amino acid sequence at least 85% identical to the 162 amino acids (SEQ ID NO: 2, ADJ25621), and which is capable of binding to an IL-21R. An IL-21 agonist has antiasthmatic, antiallergic, antiarthritic, neuroprotective, antiinflammatory, dermatological, immuno suppressive, muscular and antipsoriatic activities. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of IL-21, T helper 1 (Th1) and/or Th2, such as asthma, allergy, rheumatoid arthritis, multiple sclerosis, lupus, diabetes, Crohn's disease, psoriasis and myasthenia gravis. The present sequence represents human IL-21, which is used in the exemplification of the present invention.

XX SQ sequence 162 AA;

Db 30 OGDRHMIRQLIDIVDQKNTVNLYPEFLPAPEDVETNCWSAFSCFQKQKSANT 89  
 ID ADM41017; standard; protein; 162 AA.  
 XX AC ADM41017;  
 XX DT 15-JUL-2004 (first entry)  
 DE Human IL-21 amino acid sequence, seq id 2.  
 XX KW antiallergic; antiasthmatic; antiparasitic; antiinflammatory; anthelmintic; dermatological; immunomodulator; interleukin; IL-21; eosinophil; allergic; parasitic; asthma; allergic rhinitis; helminthic infection.  
 XX OS Homo sapiens.  
 XX FR Key Location/Qualifiers  
 PT Region 30...162 /note= "region specifically referred to in claims"  
 XX PR 13-OCT-2003; 2003WO-DK000691.  
 PR 11-OCT-2002; 2002DK-00001546.  
 PR 16-OCT-2002; 2002DK-00001587.  
 PR 17-OCT-2002; 2002US-0419225P.  
 XX PN WO2004032953-A1.  
 XX PD 22-APR-2004.  
 XX PI Romer J, Moller NPH, Skak K;  
 XX DR WPI; 2004-340821/31.  
 XX PT Use of Interleukin-21 for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, e.g. allergic conditions and/or parasitic diseases.  
 XX PS Claim 6; SEQ ID NO 2; 32PP; English.  
 XX CC The invention relates to an interleukin (IL)-21 that is used for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, e.g. allergic conditions and/or parasitic diseases. Methods of the invention are useful for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, such as allergic conditions (e.g. asthma, allergic rhinitis or allergic diseases of the skin) and/or parasitic diseases, especially helminthic infection. The current sequence represents the DNA sequence encoding IL-21. Note: This sequence is not encoded by that of ADM41016, which we are told in the specification is the IL-21 encoding nucleotide.  
 CC SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 8; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 QHLSRTGSEDS 134  
 ||||| ||||| |||||  
 Db 150 QHLSRTGSEDS 162

RESULT 15  
 ADM41017; ID ADM41017 standard; protein; 162 AA.  
 XX AC ADM41017;  
 XX DT 15-JUL-2004 (first entry)  
 DE Human IL-21 amino acid sequence, seq id 2.  
 XX KW antiallergic; antiasthmatic; antiparasitic; antiinflammatory; anthelmintic; dermatological; immunomodulator; interleukin; IL-21; eosinophil; allergic; parasitic; asthma; allergic rhinitis; helminthic infection.  
 XX OS Homo sapiens.  
 XX FR Key Location/Qualifiers  
 PT Region 30...162 /note= "region specifically referred to in claims"  
 XX PR 13-OCT-2003; 2003WO-DK000691.  
 XX PR 11-OCT-2002; 2002DK-00001546.  
 XX PR 16-OCT-2002; 2002DK-00001587.  
 XX PR 17-OCT-2002; 2002US-0419225P.  
 XX PN (NOVO ) NOVO NORDISK AS.  
 XX PA  
 XX PI Romer J, Moller NPH, Skak K;  
 XX DR WPI; 2004-340821/31.  
 XX PT Use of Interleukin-21 for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, e.g. allergic conditions and/or parasitic diseases.  
 XX PS Claim 6; SEQ ID NO 2; 32PP; English.  
 XX CC The invention relates to an interleukin (IL)-21 that is used for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, e.g. allergic conditions and/or parasitic diseases. Methods of the invention are useful for the treatment of diseases or conditions where eosinophils are involved in a protective response in a subject, such as allergic conditions (e.g. asthma, allergic rhinitis or allergic diseases of the skin) and/or parasitic diseases, especially helminthic infection. The current sequence represents the DNA sequence encoding IL-21. Note: This sequence is not encoded by that of ADM41016, which we are told in the specification is the IL-21 encoding nucleotide.  
 CC SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 8; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDPRHRMIRQLIDIVDQKNTVNLYPEFLPAPEDVETNCWSAFSCFQKQKSANT 61

Qy 2 QSDQRHMRMQLDIDVQKNTVNDLJPEFLPAPEDVETNCWSAFCQFQALKSANT 61  
Db 30 QSDQRHMRMQLDIDVQKNTVNDLJPEFLPAPEDVETNCWSAFCQFQALKSANT 89  
Qy 62 GNNERIINNSIKLKRRKRPSTNAGRRQKRHLTCFSCDSYEKKPKFELRFKSLQMIH 121  
Db 90 GNNERIINNSIKLKRRKRPSTNAGRRQKRHLTCFSCDSYEKKPKFELRFKSLQMIH 149  
Qy 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

Search completed: August 14, 2006, 21:46:36  
Job time : 198 secs

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Gencore version 5.1.9  
Sequence: 1 MQGQDRHMRMQLIDIVDQ.....LLQKMIHOHLSSRTHGSEDS 134

Run on: August 14, 2006, 21:46:53 ; Search time 39 Seconds  
(without alignments)  
Scoring table: Biostar62  
Searched: 283416 seqs., 96216763 residues

Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

\* SUMMARIES

Result No. Score Query Match Length DB ID Description

1 94.5 13.3 162 1 A53484 interleukin-15 precursor - green monkey  
2 91.5 12.9 567 2 S29498 Lymphocyte antigen  
3 82 11.5 607 1 ABX172 74K albumin precursor  
4 79 11.1 206 2 S42882 hypothetical protein  
5 78 11.0 741 2 JCT822 isocitrate dehydrogenase  
6 75.5 10.6 336 2 S42832 Fit-1S protein pre  
7 74 10.4 2197 2 BT160 FUSCA PROTEIN FUS6 variant-specific 8  
8 74 10.4 162 2 I49124 interleukin-15 - m  
9 73.5 10.3 472 2 ISQ-K54 - human  
10 73.5 10.3 868 2 T31527 hypothetical protein  
11 73 10.3 100 2 A32108 translation initiation  
12 73 10.3 304 2 T00372 hypothetical protein  
13 73 10.3 848 2 T00372 hypothetical protein  
14 72.5 10.2 309 2 T41899 hypothetical protein  
15 72.5 10.2 674 2 S61181 formin isoform IV  
16 72.5 10.2 1101 2 T26919 conserved hypothetical protein  
17 72.5 10.2 1206 2 S24407 probable methyl transferase  
18 72 10.1 257 2 C62230 N-Alternative names: 38.5K T1 glycoprotein; ST2L protein  
19 72 10.1 262 2 T29588 C;Species: Mus musculus (house mouse)  
20 72 10.1 262 2 T31813 C;Accession: S29498; A33541; S17657; S07054  
21 71.5 10.1 195 2 S42022 R;Yangisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tominaga, S.  
22 71 10.1 741 2 A83317 P;BBS Lett. 318, 83-87, 1993  
23 71 10.0 321 2 T64352 A;Title: Presence of a novel primary response gene ST2L, encoding a product highly similar to the 38.5K T1 glycoprotein.  
24 71 10.0 406 2 T28577 A;Reference number: S29498; MUID:93170492; PMID:7916701  
25 71 10.0 719 2 T22977 A;Accession: S29498  
26 71 10.0 805 2 A46266 A;Status: preliminary  
27 71 10.0 864 2 T08575 A;Molecule type: mRNA  
28 71 10.0 899 2 B38529 A;Residues: 1-1567 <YAN>  
29 71 10.0 1291 2 T22382 A;Cross-references: UNIPROT:PI4719; UNIPARC:UPI0000029617; EMBL:D13695; NID:9286100; PID:R;Klemenz, R.; Hoffmann, S.; Werenstiel, A.K.

30 71 10.0 2206 2 G7161 hypothetical protein - hu  
31 71 10.0 2924 2 T18378 variant-specific protein - hu  
32 70.5 9.9 352 2 C86294 T2D18.7 protein - hu  
33 70.5 9.9 447 2 S39316 CA3b protein - hu  
34 70.5 9.9 477 2 S21049 calcium channel protein  
35 70.5 9.9 482 2 S41211 voltage-dependent  
36 70.5 9.9 484 2 S39315 CA3a protein - hu  
37 70.5 9.9 484 2 A466508 voltage-dependent  
38 70.5 9.9 565 2 G89878 conserved hypothetical protein  
39 70 9.8 403 2 S71356 glucocorticoid-activated sensor histidine kinase  
40 70 9.8 405 2 A72383 hypothetical protein B0361.3 [i  
41 70 9.8 425 2 T50555 PR12.12 protein -  
42 70 9.8 1222 2 C88504 hypothetical protein  
43 70 9.8 1366 2 B86292 PR12.12 protein -  
44 69.5 9.8 380 2 T28454 hypothetical protein  
45 69.5 9.8 864 2 S60441 hypothetical protein

ALIGMENTS

RESULT 1

A53484

C;Species: Cercopithecus aethiops (green monkey, grivet)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
R;Grabstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Beer, J.G.; Giri, J.G.; Science 264, 965-968, 1994  
A;Title: Cloning of a T cell growth factor that interacts with the beta chain of the integrin  
A;Reference number: A53484; MUID:94233380; PMID:8178155  
A;Accession: A53484  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-162 <GRA>  
A;Cross-references: UNIPROT:P40221; UNIPARC:UPI0000031AC6; GB:U03099; NID:9493521; PID:N149-162/Product: interleukin-15 #status predicted <MAT>  
A;Note: the complete translation is not shown  
C;Superfamily: interleukin-15  
C;Keywords: growth factor  
F:83-113, 90-136/disulfide bonds: #status predicted  
F:83-113, 90-136/disulfide bonds: #status predicted

Query Match Best Local Similarity 13.3%; Score 94.5; DB 1; Length 162;  
Matches 30; Conservative 25.9%; Preq. No. 0.11; Indels 15; Gaps 5;

QY OY

Db 51 UNV3DLICK-TEDLIQSMHDATLYTESDVPHPSCKVAMKCFLLEQVISHESGGDTIH 109

QY 66 RIINVSKGLKRKPSTNAGRKHRITCPSCDSYKEKKPPLERPLKSLOQMH 121

Db 110 TVENTLIL--LANNILSNGNTIES--GCKCQEELBEKNIKFERLQSTVHIVQMPIN 160

RESULT 2

S29498

Lymphocyte antigen Ly84 precursor - mouse  
N;Alternative names: 38.5K T1 glycoprotein; ST2L protein  
C;Species: Mus musculus (house mouse)  
C;Accession: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
R;Yangisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tominaga, S.  
P;BBS Lett. 318, 83-87, 1993  
A;Title: Presence of a novel primary response gene ST2L, encoding a product highly similar to the 38.5K T1 glycoprotein.  
A;Reference number: S29498; MUID:93170492; PMID:7916701  
A;Accession: S29498  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1567 <YAN>  
A;Cross-references: UNIPROT:PI4719; UNIPARC:UPI0000029617; EMBL:D13695; NID:9286100; PID:R;Klemenz, R.; Hoffmann, S.; Werenstiel, A.K.

proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989  
 A;Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to  
 A;Reference number: A33541; MUID: 89345536; PMID: 2527364  
 A;Accession: A33541  
 A;Molecule type: mRNA  
 A;Residues: 1-191; 'V', 193-328, 'SKECPHIA' <KLE>  
 A;Cross-references: UNIPARC:UPI000028A98; GB:M24B43; NID:9201103; PIDN:AAA40160.1; PID:  
 R;Tominga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.  
 J. Mol. Biol. 199, 83-93, 1991  
 A;Title: Molecular cloning of the murine *St2* gene. Characterization and chromosomal map  
 A;Reference number: S17657; MUID:91355215; PMID:1832015  
 A;Accession: S17657  
 A;Status: translation not shown  
 A;Residues: 1-191; 'V', 193-328, 'SKECPHIA' <TOM>  
 A;Cross-references: UNIPARC:UPI000028A98; EMBL:X60184; NID:954200; PIDN:CAA42742.1; PID:  
 R;Tominga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.  
 FEBS Lett. 258, 301-304, 1989  
 A;Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly similar to the product of the mouse *St2* gene  
 A;Reference number: S07054; MUID:90092495; PMID:2532153  
 A;Accession: S07054  
 A;Molecule type: mRNA  
 A;Residues: 1-328, 'SKECPHIA' <TO2>  
 A;Cross-references: UNIPARC:UPI000003FD2; EMBL:Y07519; NID:955517; PIDN:CAA68812.1; PID:  
 C;Genetics:  
 A;Note: it is uncertain whether Met-1, Met-7 or Met-19 is the initiator  
 C;Gene:  
 A;Map position: 1  
 A;Introns: 27/1; 97/2; 155/3; 210/1; 233/1; 280/2  
 C;Superfamily: integrin  
 C;Keywords: glycoprotein  
 F;1-25/Domain: signal sequence #status predicted <SIG>  
 F;27-337/Domain: signal sequence #status predicted <MAN>  
 F;60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status  
 Query Match  
 Best Local Similarity 12.9%; Score 91.5; DB 2; Length 567;  
 Matches 33; Conservative 20; Mismatches 39; Indels 37; Gaps 7;  
 Qy 19 DQKLVVNDLVPFLPAPEDVTCNSAFSAFSQKAQIQLKSANTGNNERRINNSIKKKRK 78  
 Db 76 DRKLK-----FLPARVE----DGIYACV---IRSPNL-NKGILYLNTHK--K 113  
 Qy 79 PPSNTN-----AGRRQKRHLTCPSDCSYEKPKPFLERPKSLQKMQMIHQH----- 123  
 Db 114 PPSCNTIPDYLMLYSTVRGSSDKNFKKTCTPTIDLWNTAPVOWFKNCALKQEPFRRAHSYLF 173  
 Qy 124 IDSRTHGSE 132  
 Db 174 IDNVTHDDE 182

RESULT 3 ABXL72  
 74K albumin precursor - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C;Accession: B41682; S02693; A05288  
 C;Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic acid  
 e during development.  
 A;Reference number: A41682; MUID:89313788; PMID:2747653  
 A;Accession: B41682  
 A;Molecule type: mRNA  
 A;Residues: 3-607 <MO5>  
 A;Cross-references: UNIPROT:P1872; UNIPARC:UPI0001714FB; GB:M21442; NID:9213930; PIDN:  
 R;Schorpp, M.; Doebelein, U.; Wagner, U.; Ryffel, G.U.  
 J. Mol. Biol. 199, 83-93, 1988  
 A;Title: 5'-flanking and 5'-proximal exon regions of the two *Xenopus* albumin genes. Dele  
 A;Reference number: S02692; MUID:88172470; PMID:2451026  
 A;Accession: S02693  
 A;Status: not compared with conceptual translation

RESULT 4 S49882  
 Hypothetical protein YIL127c - yeast (*Saccharomyces cerevisiae*)  
 N1Alternate names: hypothetical protein YIL127c  
 C;Species: *Saccharomyces cerevisiae*  
 C;Date: 13-Jan-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S49882  
 R;Hamlyn, N.; Churcher, C.  
 Submitted to the EMBL Data Library, November 1994  
 A;Reference number: S49881  
 A;Accession: S49882  
 A;Molecule type: DNA  
 A;Residues: 1-206 <HAM>  
 A;Cross-references: UNIPROT:P40470; UNIPARC:UPI00013B441; GB:Z47047; EMBL:Z46833; NID:946  
 C;Genetics:  
 A;Gene: MIR-YIL127c  
 A;Cross-references: SGD:S0001389  
 A;Map position: 9L

Query Match  
 Best Local Similarity 11.1%; Score 79; DB 2; Length 206;  
 Matches 29; Conservative 26.1%; Pred. No. 3.9; Mismatches 48; Indels 16; Gaps 3;  
 Qy 20 QKLVVNDLVPFLPAPEDVTCNSAFSAFSQKAQIQLKSANTGNNERRINNSIKKKRK 79  
 Db 12 QATSVNGLNLPLPGVPLVNGKTSVNGSKAQDILRMLKVKVQLOPNDVHKKKC 71

Qy 80 PSTNAGRQRKHLTCPSDCSYEKPKPFLERP--RSLLQKMIHQHLSST 128

|  |   |
|--|---|
| Db   | 72 KLVKKKVKVKHKL-----DKEQLEQAKHQVLLK--HQBCTLT 108   |
| RESULT 5   | <p>JC7822 isocitrate dehydrogenase (NADP)<sup>+</sup> (EC 1.1.1.42), monomeric type - Azotobacter vinelandii C;Species: Azotobacter vinelandii<br/>C;Date: 03-Jun-2002 #text_change 09-Jul-2004<br/>C;Accession: JC7822; PC7187<br/>R;Sahara, T.; Takada, Y.; Takeuchi, Y.; Yamada, N.; Fukunaga, N.<br/>R;Ciriaco, Biotechnol. Biotechol., 66, 499-500, 2002<br/>A;Title: Cloning, sequencing, and expression of a gene encoding the monomeric isocitrate A;Reference number: JC7822; PMID:12005040; MUID:2199801<br/>A;Reference: 1-741 &lt;SAH&gt;<br/>A;Molecule type: protein<br/>A;Residues: 2-16 &lt;SA2&gt;<br/>A;Cross-references: UNIPARC:UPI000017CDPS<br/>A;Comment: This enzyme that catalyzes the oxidative decarboxylation of isocitrate to α-ketoglutarate is typical monomeric, it contributes to the respiratory protection of nitro bacteria.</p>  |
| C;Keywords:  | A;Gene: icd<br>A;Superfamily: isocitrate dehydrogenase, monomeric type<br>C;Keywords: oxidoreductase  |
| Query Match  | 11.0%; Score 78; DB 2; Length 141;  |
| Best Local Similarity  | 24.8%; Pred. No. 18;  |
| Matches  | 26; Conservative 23; Mismatches 34; Indels 22; Gaps 4;  |
| Qy   | 5 DRHMTRMRQLIDIVDQLKNYVNDL-----VPEFLPAPEDVETNCWSAFSCFQKAOLKS 58   |
| Db   | 77 DANILKLPNTISASVPLQKAATKELQOGSYKUPDY--PEEPKTDTEDKVARYDKIGSA 133   |
| Qy   | 59 AN---TGNERRITINNSIKUKRKKEPPSTNAGRRQKRHLTCPSCCDS 99   |
| Db   | 134 VNPVLREGNSDERRAPLSPVNQVARKHP-----HRKGAWSDS 169  |
| RESULT 6   | <p>S12632 FIT-15 protein precursor - rat<br/>C;Species: Rattus norvegicus (Norway rat)</p>  |
| C;Date:  | 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004   |
| C;Accession:   | S42632  |
| C;Bergers, G.; Rekerstorfer, A.; Braselmann, S.; Graninger, P.; Busslinger, M. |   |
| A;Title:   | Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA isoforms with different properties   |
| A;Reference number:  | S42632; MUID:94178260; PMID:831748  |
| A;Status:  | preliminary   |
| A;Molecule type:   | mRNA  |
| A;Residues:  | 1-336 <BER>   |
| A;Cross-references:  | UNIPROT:Q62611; UNIPARC:UPI00002AC15; GB:U04319; NID:9488278; PMID:15300000   |
| C;Superfamily:   | vaccinia virus B15 protein; immunoglobulin homology   |
| Query Match  | 10.6%; Score 75.5; DB 2; Length 336;  |
| Best Local Similarity  | 22.2%; Pred. No. 14;  |
| Matches  | 30; Conservative 26; Mismatches 42; Indels 37; Gaps 6;  |
| Qy   | 15 IDIVDQQLQNTVNDLVP-----EFLPADEDVETNCWSAFSCFQKAOLKSAN 60   |
| Db   | 49 INPVWVYWSVNERIPTQKRNRIFVSRDRXELPKAV 102  |
| Qy   | 61 TGNNERRITINNSIKUKRKPP-----STNAGRQKRHLTCPSCCDSYKKRPFLE 110  |
| Db   | 103 TGS---LNVTYK--RPPENCKIPDYMMSVTGDSDRNSKTCPTITALYNWTAPQWPK 155  |
| Qy   | 111 RFKSLQLQMIHQHLS 125   |
| RESULT 7   | <p>T47906 FUSCA PROTEIN FUS6 - Arabidopsis thaliana<br/>N;Alternate names: protein T20K12.40<br/>C;Species: Arabidopsis thaliana (mouse-ear cress)<br/>C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004<br/>C;Accession: T47906<br/>R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Reference number: 224480<br/>A;Accession: T47906<br/>A;Status: preliminary<br/>A;Molecule type: DNA<br/>A;Residues: 1-440 &lt;DEH&gt;<br/>A;Experimental source: cultivar Columbia; BAC clone T20K12<br/>C;Genetics:<br/>A;Map position: 3<br/>A;Introm: 130/3; 237/3; 278/1; 304/2; 382/3<br/>A;Note: T20K12.40<br/>C;Superfamily: COR9 signalosome complex subunit 1</p>  |
| Query Match  | 10.4%; Score 74; DB 2; Length 440;  |
| Best Local Similarity  | 22.0%; Pred. No. 25;  |
| Matches  | 26; Conservative 22; Mismatches 50; Indels 20; Gaps 3;  |
| Qy   | 6 RMHMRMRQLIDIVDQLKNYVNDL-----VPEFLPAPEDVETNCWSAFSCFQKAOLKSANTVGNNE 65  |
| Db   | 230 KYKLAARKFLDVNLPELGNSYNEVI----AQDQIATYGGHACALASFDRSIIKAF----- 278  |
| Qy   | 66 RIRNVSIIKUKRKKEPPSTNAGRRQKRHLTCPSCCDSYEKKUPPKFILERFKSIIQKMHQH 123  |
| Db   | 279 -IDININFRNPFLELYPDVREBLINDYFSSRYASC-----LEYLASLKSNIILDLHL 327   |
| RESULT 8   | <p>B11600 variant-specific surface protein 1 homolog PPB1055c - malaria parasite (Plasmodium falciparum)<br/>N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)<br/>C;Species: Plasmodium falciparum<br/>C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004<br/>C;Accession: B71600<br/>R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Perreira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998<br/>A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.<br/>A;Reference number: A71600; MUID:99021743; PMID:980551<br/>A;Accession: B71600<br/>A;Status: preliminary; nucleic acid sequence not shown; translation not shown<br/>A;Molecule type: DNA<br/>A;Residues: 1-2197 &lt;GAR&gt;<br/>A;Cross-references: UNIPROT:O96296; UNIPARC:UPI00001796B2; GB:AB00134; GB:AE001362; NID:15300000<br/>C;Genetics:<br/>A;Experimental source: clone 3D7<br/>A;Gene: PPB1055c</p> |
| Query Match  | 10.4%; Score 74; DB 2; Length 2197;   |
| Best Local Similarity  | 29.5%; Pred. No. 1.4e+02;   |
| Matches  | 28; Conservative 16; Mismatches 41; Indels 10; Gaps 4;  |
| Qy   | 21 LKNVNDLVPFELPADEDVETNCWSAFSCFQKAOLKSANTNGNERITINNSIKUKRK 78  |
| Db   | 1594 VKSPLTWIPK-TAVNNDPQDNVILSKFCNSCGSASATISTN-GNEBDADICMKGLEK 1651   |
| Qy   | 79 -----PRSTNAGRRQKRHLTCPSCCDSYKKRPFLE 107  |
| Db   | 1652 DECKRKPGEGNSGOTCNELTLHPLDVQDEDPLEE 1686  |
| RESULT 9   |   |

149124  
interleukin-15 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 09-Jul-2004  
C;Accession: 149124  
R;Anderson, D.M.; Johnson, L.; Glaccum, M.B.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.  
Genomics 25, 701-706, 1995  
A;Title: Chromosomal assignment and genomic structure of IL115.  
A;Reference number: A56005; MUID:95278940; PMID:7759105  
A;Accession: 149124  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-162 <REBS>  
A;Cross-references: UNIPROT: P48346; UNIPARC:UPI0000019C8; EMBL:U14332; PIDN:984941; PIID:1117202; PIDN:CA855073.1  
A;Gene: IL15  
C;Superfamily: interleukin-15

RESULT 10

ISG-K54 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004  
C;Accession: 159087  
R;Levy, D.; Larner, A.; Chaudhuri, A.; Babiss, L.E.; Darnell, J.E.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8929-8933, 1986  
A;Title: Interferon-stimulated transcription: isolation of an inducible gene and identification  
A;Reference number: 159087; MUID:87067427; PMID:3466167  
A;Accession: 159087  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-172 <REBS>  
A;Cross-references: UNIPROT: P08913; UNIPARC:UPI000012D3E4; GB:ML4660; PIDN:9186559; PIDN:  
C;Genetics: GDB:IF154; G10P2; IF1-54  
A;Cross-references: GDB:119959; OMIM:147040  
A;Map position: 10q3-10q24  
C;Superfamily: interferon-induced 56K protein

Query Match Best Local Similarity 10.3%; Score 73.5; DB 2; Length 162;  
Matches 22; Conservative 19.8%; 30; Mismatches 54; Indels 5; Gaps 3;

Qy 15 IDI--VDQLQVYNDL-VPERFLPAPDVETNCWMSAFSCFOKAOLKSANTONNERIINV 70  
Db 51 IDVRYDLEKIESLIOSIHIDTTLTYTDSDPHRSCKVTAMNCF-LLELOVILHYSNTLINE 109

Qy 71 SIKKLKKRKPSTNAQRQRQKRHLTCPCSDSYEKKPKPFERFKSLIQRMNH 121  
Db 110 TVRNVLYLANSTLSNKVAEKGCKCEBEBLKTFIFLQSFIRIVQMPIN 160

RESULT 11

ISG-K54 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004  
C;Accession: 159087  
R;Levy, D.; Larner, A.; Chaudhuri, A.; Babiss, L.E.; Darnell, J.E.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8929-8933, 1986  
A;Title: Interferon-stimulated transcription: isolation of an inducible gene and identification  
A;Reference number: 159087; MUID:87067427; PMID:3466167  
A;Accession: 159087  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-172 <REBS>  
A;Cross-references: UNIPROT: P08913; UNIPARC:UPI000012D3E4; GB:ML4660; PIDN:9186559; PIDN:  
C;Genetics: GDB:IF154; G10P2; IF1-54  
A;Cross-references: GDB:119959; OMIM:147040  
A;Map position: 10q3-10q24  
C;Superfamily: interferon-induced 56K protein

Query Match Best Local Similarity 10.3%; Score 73.5; DB 2; Length 162;  
Matches 22; Conservative 19.8%; 30; Mismatches 54; Indels 5; Gaps 3;

Qy 16 7 RMRMQLQDITVQDQLQVYNDL-VPERFLPAP--EDVETNC--WS-----AFSC 50  
Db 106 HNGRLSDVQIVYDKVKR----VCEKSSSPRIESPBLCBERGWIRLKGGQNQNERAKVC 160

Qy 51 FOKAQQLKSANTGNERNERINNSKKRKPSTNA--GRQRQKRHLTCPCSDSYEKKPKPF 108  
Db 161 FEKALSKKKPKNPEFTSGLATASYRDLNWPSONAIDPLQARL-----NPDNQY 210

Qy 109 LERPKSILQKOMTHQHLSRTHQSE 133  
Db 211 L---KVLLALKHK--MRESGEE 229

RESULT 11

hypothetical protein Y47D3A.14 - Caenorhabditis elegans  
T31527

RESULT 12

A32108  
translation initiation factor eif-2 alpha chain - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein J429; protein YJR007w  
C;Species: Saccharomyces cerevisiae  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C;Accession: A32108; S55195; S57022  
R;Cigan, A.M.; Pabich, E.K.; Feng, L.; Donahue, T.P.  
Proc. Natl. Acad. Sci. U.S.A. 86, 2784-2788, 1989  
A;Title: Yeast translation initiation suppressor sui2 encodes the alpha-subunit of eukaryotic initiation factor 2  
A;Reference number: A32108; MUID:89202411; PMID:2649894  
A;Accession: A32108  
A;Molecule type: DNA  
A;Residues: 1-104 <CG>  
A;Cross-references: UNIPROT: P20459; UNIPARC:UPI00000530CA; EMBL:M25552; PIDN:9341369; PIDN:  
R;de Haan, M.; Smits, P.H.M.; Grivell, L.A.  
R;de Haan, M.; Grivell, L.A.; Smits, P.H.M.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: S55183  
A;Accession: S55195  
A;Molecule type: DNA  
A;Residues: 1-104 <DH>  
A;Cross-references: UNIPARC:UPI00000530CA; EMBL:X87611; PIDN:9854567; PIDN:CAA60929.1; PIDN:  
R;de Haan, M.; Grivell, L.A.; Smits, P.H.M.  
submitted to the Protein Sequence Database, September 1995  
A;Reference number: S56771  
A;Accession: S57022  
A;Molecule type: DNA  
A;Residues: 1-1304 <ZAG>  
A;Cross-references: UNIPARC:UPI00000530CA; EMBL:Z49507; PIDN:91015631; PIDN:CAA89529.1; PIDN:  
C;Genetics: SGD:SUI2  
A;Cross-references: SGD:S0003767; MIPS:XUR007w  
A;Map position: 10R  
C;Superfamily: translation initiation factor eif-2 alpha chain  
C;Keywords: phosphoprotein; protein biosynthesis

Query Match Best Local Similarity 10.3%; Score 73; DB 2; Length 304;  
Matches 34; Conservative 24.8%; 56; Mismatches 56; Indels 22; Gaps 7;

Qy 16 DIVDQLQVYNDL-VPERFLPAPDVETNC-BMSAFSCFOKAOLKSANTGNERNERINNSKKRKPSTNA--GRQRQKRHLTCPCSDSYEKKPKPF 172  
Db 164 DVLDLKNYISKRLTQAVKRADEVUSCSFYEGLDAKDA-LKSAEDMSTQMOKVLU 222

|  | Matches | Conservative  | Mismatches | Indels | Gaps |
|--|---------|---|------------|--------|------|
| Qy   | 73      | KUKRKPPSTNAGRRQRKHLTCSSCDSYE-----KPKPFLEPKSLIQ                | 117        |        | 6;   |
| Db   | 223     | VAAPFLVYLTQALDKQKGIEQLES--AIEKITEVITKYGGVCNTMPPKAVTATEDAQ     | 280        |        |      |
| Qy   | 118     | KMTH-OHSSRTGSED 133   |            |        |      |
| Db   | 281     | ALLESKELDNRSDSEDD 297   |            |        |      |
| RESULT 13  |         |   |            |        |      |
| T00372   |         | hypothetical protein KIAA0650 - human (fragment)              |            |        |      |
| C;Species: Homo sapiens (man)  |         |   |            |        |      |
| C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004              |         |   |            |        |      |
| C;Accession: T00372; T12523  |         |   |            |        |      |
| R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. |         |   |            |        |      |
| DNA Res. 5, 169-176, 1998  |         |   |            |        |      |
| A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete |         |   |            |        |      |
| A;Reference number: Z14142; MUID:98403880; PMID:9734811                                  |         |   |            |        |      |
| A;Status: preliminary; translated from GB/EMBL/DDBJ                                      |         |   |            |        |      |
| A;Molecule type: mRNA  |         |   |            |        |      |
| A;Residues: 1-848 <ISH>  |         |   |            |        |      |
| A;Cross-references: UNIPROT:O75141; UNIPARC:UPI00006CBB7; EMBL:AB014550; NID:9327113;    |         |   |            |        |      |
| A;Experimental source: brain   |         |   |            |        |      |
| A;Residues: E, 122-348 <WAM>   |         |   |            |        |      |
| A;Cross-references: UNIPARC:UPI000072B1B; EMBL:AL080138                                  |         |   |            |        |      |
| A;Experimental source: adult testis; clone DKFZp434K063                                  |         |   |            |        |      |
| A;Genetics:  |         |   |            |        |      |
| A;Note: KIA0650; DKFZp434K063.1  |         |   |            |        |      |
| Query Match  | 10.3%   | Score 73; DB 2; Length 848;                                   |            |        |      |
| Best Local Similarity  | 25.5%   | Pred. No. 62; Mismatches 47; Indels 10; Gaps 5;               |            |        |      |
| Matches  | 27;     | Conservative 22; Mismatches 47; Indels 10; Gaps 5;            |            |        |      |
| Qy   | 31      | ERLPPAPRDPVETNC-EWSAFSCFKQAKLSANTGNERNIRINVSIKKLKRKPPSTNAGRRQ | 89.        |        |      |
| Db   | 66      | KRIPGPGENKDLQFTWREFSDFIRVQLIS--GPPAKULLIDMPPELKESEPVIN-GRDLQ  | 121        |        |      |
| Qy   | 90      | HRLTCPSDSYEVKKPKEPLERKSLQKMIHQH--SSRTGSED 133                 |            |        |      |
| Db   | 122     | NPIIVQLOQDWNPAP--VQYKISLTKASNLKLMPSNOHQHDE 164                |            |        |      |
| RESULT 14  |         |   |            |        |      |
| T41889   |         |   |            |        |      |
| PE38 orf153 - Bombyx mori nuclear polyhedrosis virus (isolate T3)                        |         |   |            |        |      |
| C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV                                |         |   |            |        |      |
| A;Variety: isolate T3  |         |   |            |        |      |
| C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004              |         |   |            |        |      |
| C;Accession: T41889  |         |   |            |        |      |
| R;Gomi, S.; Maijima, K.; Meda, S.  |         |   |            |        |      |
| J. Gen. Virol. 80, 1323-1337, 1999   |         |   |            |        |      |
| A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.            |         |   |            |        |      |
| A;Reference number: 222020; MUID:99281911; PMID:10355780                                 |         |   |            |        |      |
| A;Accession: T41889  |         |   |            |        |      |
| A;Status: preliminary; translated from GB/EMBL/DDBJ                                      |         |   |            |        |      |
| A;Molecule type: DNA   |         |   |            |        |      |
| A;Residues: 1-309 <KAM>  |         |   |            |        |      |
| A;Cross-references: UNIPROT:O92504; UNIPARC:UPI0000P20C2; EMBL:L33180; NID:93745835; PI  |         |   |            |        |      |
| A;Experimental source: isolate T3  |         |   |            |        |      |
| C;Genetics:  |         |   |            |        |      |
| A;Note: pe38   |         |   |            |        |      |
| C;Superfamily: Orgyia pseudotsugata nuclear polyhedrosis virus PE-38 protein             |         |   |            |        |      |
| Query Match  | 10.2%   | Score 72.5; DB 2; Length 309;                                 |            |        |      |
| Best Local Similarity  | 23.4%   | Pred. No. 24;   |            |        |      |

Search completed: August 14, 2006, 21:52:27  
Job time : 42 secs

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IL21\_PIG STANDARD; PRT; 146 AA.  
 ID IL21\_PIG OC  
 AC 076106; OC  
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot. OC  
 DT 23-NOV-2004, sequence version 2. OC  
 DT 07-FEB-2006, entry version 12. OC  
 DE Interleukin-21 precursor (IL-21). RC  
 GN Name=IL21; RA  
 OS NCBI\_TAXID=9523; RA  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; RA  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; RA  
 OC Sus. RA  
 OC NCBITAXID=9823; RA  
 RN [1] R  
 RP NUCLEOTIDE SEQUENCE [mRNA]. RT  
 RX PubMed=1510555; DOI=10.1289/jvmb.66.269; RL  
 RA Muneta Y., Kikuma R., Uenishi H., Hoshino T., Yoshihara K., Tanaka M., CC  
 RA Hamashita N., Mori Y.; Submitted (DRC-2003) to the EMBL/Genbank/DBJ databases. CC  
 "Molecular cloning, expression and biological function of porcine CC  
 RT interleukin-21." CC  
 J. Vet. Med. Sci. 66:269-275 (2004). CC  
 -!- FUNCTION: Cytokine with immunoregulatory activity. May promote the CC  
 transition between innate and adaptive immunity. Induces the CC  
 production of IgG(1) and IgG(3) in B-cells. May play a role in CC  
 proliferation and maturation of natural killer (NK) cells in CC  
 synergy with IL15. May regulate proliferation of mature B- and T- CC  
 cells in response to activating stimuli. In synergy with IL15 and CC  
 IL18 stimulates interferon gamma production in T-cells and NK CC  
 cells (By similarity). During T-cell mediated immune response may CC  
 inhibit dendritic cells (DC) activation and maturation. CC  
 -!- SUBCELLULAR LOCATION: Secreted protein (By similarity). CC  
 -!- SIMILARITY: Belongs to the IL-21 family. CC  
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 EMBL; AB07020; BAD1128.1; ALT\_INIT; mRNA. CC  
 KW Cytokine; Signal. CC  
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 DR EMBL; AB07020; BAD1128.1; ALT\_INIT; mRNA. CC  
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 DR Ensembl; ENSCAFGB0000004004; Canis familiaris. CC  
 KW Cytokine; Signal. CC  
 FT SIGNAL 1 17 Potential. CC  
 FT CHAIN 18 147 Interleukin-21. CC  
 FT /PRID=PRO\_0000015504. CC  
 FT DISULFID 64 115 Potential. CC  
 FT DISULFID 71 118 Potential. CC  
 SQ SEQUENCE 146 AA; 16776 MW; PRB8D9836AF219AA CRC64; CC  
 Query Match Best Local Similarity 72.2%; Score 513; DB 1; Length 146; CC  
 Matches 100; Conservative 7; Mismatches 17; Indels 0; Gaps 0; CC  
 QY 2 QGODRHMTRMQLDIDVQKVNVDLVPFLPAPEDVETNCWSAFCQKQQLKSANT 61 CC  
 DB 23 QGDQDRHMLRQLDIDVQKVNVDLVPFLPAPEDVETNCWSAFCQKQQLKSANT 82 CC  
 QY 62 GNNERIINVISIKLKRRKEPSTWAGRQRKHLRTCPSCSYKEKKPKEFLERFKSLQKMH 121 CC  
 DB 83 GNEQIQINVLTKQKRLKQPKPTWAGRQRKHLRTCPSCSYKEKKPKEFLERFKSLQKMH 142 CC  
 Query Match Best Local Similarity 80.6%; Score 524; DB 1; Length 146; CC  
 Matches 100; Conservative 11; Mismatches 13; Indels 0; Gaps 0; CC  
 QY 122 QHLS 125 CC  
 DB 143 QHLS 146 CC  
 RESULT 5 CC  
 IL21\_MOUSE STANDARD; PRT; 146 AA. CC  
 ID IL21\_MOUSE AC  
 AC QPESIT; CC  
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot. CC  
 DT 01-MAR-2001, sequence version 1. CC  
 DT 07-FEB-2006, entry version 24. CC  
 DB Interleukin-21 precursor (IL-21). CC  
 GN Name=IL21; GN  
 OS Mus musculus (Mouse). OS  
 OC Bucaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorphati; OC  
 OC Muridae; Muridae; Murinae; Mus. OC  
 RN [1] R  
 RP NUCLEOTIDE SEQUENCE [mRNA]. RT  
 RC STRAIN=BALB/C; RL  
 RX MEDLINE=20531754; PubMed=1081504; DOI=10.1038/35040504; RA  
 RA Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schneider S., RA  
 RA Burkhead S., Heipell M., Brandt C., Kuiper J.L., Kramer J., RA

RESULT 4  
 IL21\_CANPA STANDARD; PRT; 146 AA.  
 ID IL21\_CANPA  
 AC 061719; OC  
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot. OC  
 DT 05-JUL-2004, sequence version 1. OC  
 DT 07-FEB-2006, entry version 11. OC  
 DB Interleukin-21 precursor (IL-21). OC  
 Name=IL21; Canis familiaris (Dog). OC  
 Canis familiaris (Dog). OC  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC



RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;  
 RT Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4  
 RL CCNBS.;  
 Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Cytokine with immunoregulatory activity. May promote the transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and T-cells in response to activating stimuli. In synergy with IL15 and IL18 stimulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response may inhibit dendritic cells (DC) activation and maturation (By similarity).

--!- SUBCELLULAR LOCATION: Secreted protein (By similarity).

--!- SIMILARITY: Belongs to the IL-21 family.

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--!- EMBL; EMBL; AV247761; RAP0440.1; -; mRNA.

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL <1 10 Potential.

FT CHAIN 11 123 Interleukin-21.

FT CARBOHYD 77 77 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 56 107 Potential.

FT DISULFID 63 110 Potential.

FT NON-TER 1 1 Potential.

FT NON-TER 123 123 AA; 13945 MW; 8656CBBA95447E34 CRC64;

SQ SEQUENCE

Query Match Best Local Similarity 48.4%; Score 344; DB 1; Length 123; N-matches 65; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

OY 2 QGQDRHMRMQLDIVDQLKVNNDLVPEFLPAPEDVETNCWSAFSCKQAKLQSANTGNNERIT 61  
 15 ORPRPRLRILRLHVNLVEQDQLKVNNDLVPEFLPAPEDVETNCWSAFSCKQAKLQSANTGNNERIT 74

Db 62 GNNERIINVISIKKURKPKSTNAGRRQKRHLTCSCDSYEVKKPPKEFLE 110  
 75 GSNNRISIISDVLQIIRRUPATKAKKQQLSVLKCPSCSDSYEVKKPPKEFLE 123

RESULT 8

Q581U6 CHICK PRELIMINARY; PRT; 145 AA.

ID Q581U6\_

AC 0581U6\_-

DT 26-APR-2005, integrated into UniProtKB/TREMBL.

DT 26-APR-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.

DE Interleukin 21.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI\_TaxID=931;

RN [1] NUCLEOTIDE SEQUENCE.

RP shao J.; Dong W.; Xiang L.; Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

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CC DR EMBL; AV943313; AXA40551.1; -; mRNA.

SQ SEQUENCE 145 AA; 16637 MW; E70AB6A568CDABE6 CRC64;

Query Match Best Local Similarity 21.0%; Score 149.5; DB 2; Length 145; Mismatches 39; Conservative 20; Nmismatches 52; Indels 11; Gaps 4;

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--!- EMBL; AV247761; RAP0440.1; -; mRNA.

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL <1 10 Potential.

FT CHAIN 11 123 Interleukin-21.

FT CARBOHYD 77 77 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 56 107 Potential.

FT DISULFID 63 110 Potential.

FT NON-TER 1 1 Potential.

FT NON-TER 123 123 AA; 13945 MW; 8656CBBA95447E34 CRC64;

SQ SEQUENCE

Query Match Best Local Similarity 48.4%; Score 344; DB 1; Length 123; N-matches 65; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

OY 69 NVSIKKURKPKSTNAGRRQKRHLTCSCDSYEVKKPPKEFLE 125  
 16 DIVDQLK--NYNDLVPEFLPAPEDVETNCWSAFSCKQAKLQSANTGNNERIT 67  
 52 DVISDLKIKDQIISLHDIALTYESDWHPNCKTAMKCPLBLHVISLESKNETIHOTV 111

Db 86 FAKTWKILRPPPLVS----EEH---CESCESYERKKPQEFLNSFSKLMQKLFKNSTA 137

QY 126 SR 127

Db 138 ER 139

RESULT 9

IL15\_FELCA

ID IL15\_PELCA STANDARD; PRT; 162 AA.

AC 097687;

DT 01-MAY-1999, sequence version 1.

DT 07-FEB-2006, entry version 23.

DR Interleukin-15 precursor (IL-15).

GN Name=IL15;

OS Felis silvestris catus (Cat).

OC Butarvota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Rutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae; Felinae; Felis.

OC OX NCBI\_TaxID=9685;

[1]

RP NUCLBOTIDE SEQUENCE [mRNA].

RC

RA Barger A.B.; Dean G.A.; Lavyov A.S.; Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

RL CC -!- FUNCTION: Cytokine that stimulates the proliferation of T-lymphocytes. Stimulation by IL-15 requires interaction of IL-15 with components of IL-2R, including IL-2R beta and probably IL-2R gamma but not IL-2R alpha. (By similarity).

CC --!- SUBCELLULAR LOCATION: Secreted protein.

--!- SIMILARITY: Belongs to the IL-15 family.

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--!- EMBL; AR108148; RADD05268.1; -; mRNA.

DR Interpro; IPR003443; Interleukin\_15.

DR PANTHER; PTHR11323; Interleukin\_15; 1.

PFam; PF02372; IL15; 1.

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 29 Potential.

FT PROPER 30 48 Potential.

FT /Prid=PRO 00000015395.

FT CHAIN 49 162 Interleukin-15.

FT /Prid=PRO 0000013396.

FT CARBOHYD 104 104 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 127 127 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 83 133 Potential.

FT DISULFID 90 136 Potential.

FT SEQUENCE 162 AA; 18412 MW; D8C7CBFF40110DD CRC64;

Query Match Best Local Similarity 14.3%; Score 101.5; DB 1; Length 162; N-matches 31; Conservative 19; Mismatches 48; Indels 19; Gaps 5;

OY 68 INVISIKKURKPKSTNAGRRQKRHLTCSCDSYEVKKPPKEFLE 121  
 112 ENII-----LANSGLSNRNIETGCKECEBLSERKIKEFLOSFVHIVOMPIN 160

Db

RESULT 10

Q6RGX7\_HUMAN

|                       |  |                                    |      |         |    |     |   |   |
|-----------------------|--|------------------------------------|------|---------|----|-----|---|---|
| ID                    | Q6FGX7_HUMAN   | PRELIMINARY;                       | PRT; | 135 AA. | OY | 15  | RDIVDQLKQVNDLVLVER---LPAPEDVENCNSAFSP---OQAQKSANTGNNE   | 65  |
| AC                    | Q6FGX7;  |                                    |      |         | Db | ::: | :   :   . :   :   . :   :   . :   :   . :   :   . :   : | 24 UNIVISDLRK-IREDLQSMHDIAILYTESDVHPSCKVITAMKCPFLLELOVISLESQDASIHD 82 |
| DT                    | 10-MAY-2005,   | integrated into UniProtKB/T-REMBL. |      |         |    |     |   |   |
| DT                    | 10-MAY-2005,   | sequence version 1.                |      |         |    |     |   |   |
| DE                    | 07-FEB-2006,   | entry version 6.                   |      |         |    |     |   |   |
| DE                    | IL15 protein   | (Interleukin 15, isoform 2).       |      |         |    |     |   |   |
| GN                    | Name=IL15;   |                                    |      |         |    |     |   |   |
| OS                    | Homo sapiens (Human).  |                                    |      |         |    |     |   |   |
| OC                    | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |                                    |      |         |    |     |   |   |
| OC                    | Mammalia; Buttheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  |                                    |      |         |    |     |   |   |
| OC                    | Homo.  |                                    |      |         |    |     |   |   |
| OX                    | NCBI_TaxID=9606;   |                                    |      |         |    |     |   |   |
| RN                    | [1]  | NUCLEOTIDE SEQUENCE.               |      |         |    |     |   |   |
| RN                    | TISSUE=PCR rescued clones;   |                                    |      |         |    |     |   |   |
| RX                    | MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;   |                                    |      |         |    |     |   |   |
| RA                    | Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,   |                                    |      |         |    |     |   |   |
| RA                    | Neubert P., Kistrang K., Schatten R., Shen B., Henze S., Mar W.,   |                                    |      |         |    |     |   |   |
| RA                    | Submited (JUN-2004) to the EMBL/GenBank/DDBJ databases.  |                                    |      |         |    |     |   |   |
| RN                    | [2]  | NUCLEOTIDE SEQUENCE.               |      |         |    |     |   |   |
| RP                    | TISSUE=PCR rescued clones;   |                                    |      |         |    |     |   |   |
| RA                    | Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  |                                    |      |         |    |     |   |   |
| RA                    | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  |                                    |      |         |    |     |   |   |
| RA                    | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  |                                    |      |         |    |     |   |   |
| RA                    | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  |                                    |      |         |    |     |   |   |
| RA                    | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  |                                    |      |         |    |     |   |   |
| RA                    | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  |                                    |      |         |    |     |   |   |
| RA                    | Richards S., Worley K.C., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,   |                                    |      |         |    |     |   |   |
| RA                    | Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,   |                                    |      |         |    |     |   |   |
| RA                    | Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,  |                                    |      |         |    |     |   |   |
| RA                    | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,   |                                    |      |         |    |     |   |   |
| RA                    | Reiffel Y.-S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  |                                    |      |         |    |     |   |   |
| RA                    | Schnerech A., Schein J.B., Jones S.J.M., Marra M.A.,   |                                    |      |         |    |     |   |   |
| RT                    | "Generation and initial analysis of more than 15,000 full-length human   |                                    |      |         |    |     |   |   |
| RT                    | and mouse cDNA sequences";   |                                    |      |         |    |     |   |   |
| RL                    | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).   |                                    |      |         |    |     |   |   |
| RN                    | [3]  | NUCLEOTIDE SEQUENCE.               |      |         |    |     |   |   |
| RP                    | TISSUE=PCR rescued clones;   |                                    |      |         |    |     |   |   |
| RC                    | NIH MAC Project;   |                                    |      |         |    |     |   |   |
| RG                    | Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.   |                                    |      |         |    |     |   |   |
| RN                    | [4]  | NUCLEOTIDE SEQUENCE.               |      |         |    |     |   |   |
| RP                    | TISSUE=Colon;  |                                    |      |         |    |     |   |   |
| RA                    | Li C.;   |                                    |      |         |    |     |   |   |
| RL                    | Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  |                                    |      |         |    |     |   |   |
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| CC                    |  |                                    |      |         |    |     |   |   |
| EMBL                  | BC100962; AA100963-1; -; mRNA.   |                                    |      |         |    |     |   |   |
| DR                    | EMBL; CR54200; CAG46804.1; -; mRNA.  |                                    |      |         |    |     |   |   |
| DR                    | EMBL; AY720442; AAU21241.1; -; mRNA.   |                                    |      |         |    |     |   |   |
| DR                    | EMBL; CR541980; CAG4677.1; -; mRNA.  |                                    |      |         |    |     |   |   |
| DR                    | EMBL; BC100961; AA100962.1; -; mRNA.   |                                    |      |         |    |     |   |   |
| DR                    | Ensembl; ENSG0000164336; Homo sapiens.   |                                    |      |         |    |     |   |   |
| DR                    | GO; GO:000556; C:extracellular region; IEA.  |                                    |      |         |    |     |   |   |
| DR                    | GO; GO:005126; P:hematopoietin/interferon-class (D200-domain. . . ; IEA.   |                                    |      |         |    |     |   |   |
| DR                    | GO; GO:000955; P:immune response; IEA.   |                                    |      |         |    |     |   |   |
| DR                    | InterPro: IPR00443; Interleukin_15.  |                                    |      |         |    |     |   |   |
| DR                    | PANTHER: PTM01233; Interleukin_15; 1.  |                                    |      |         |    |     |   |   |
| DR                    | Pfam; PF02372; IL15; 1; 14912 MW; EB44F422096B143E CRC64;  |                                    |      |         |    |     |   |   |
| SQ                    | SEQUENCE 135 AA; 14912 MW;   |                                    |      |         |    |     |   |   |
| Query Match           | 14.0%; Score 99.5; DB 2; Length 135;   |                                    |      |         |    |     |   |   |
| Best Local Similarity | 25.9%; Pred. No. 0.35;   |                                    |      |         |    |     |   |   |
| Matches               | 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;   |                                    |      |         |    |     |   |   |

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., FT  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., FT  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., FT  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., FT  
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A., FT  
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., FT  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., FT  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., FT  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., FT  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smilus D.E., FT  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., FT  
 RA "Generation and initial analysis of more than 15,000 full-length human FT  
 and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). FT  
 RN [7])

RP NUCLEOTIDE SEQUENCE OF 49-162. FT  
 RL TISSUE=Epidermis; FT  
 RA Sorel M.A., Jacques Y.; FT  
 RA "IL15 expression in human keratinocytes"; FT  
 RL Submitted (Oct-1994) to the EMBL/GenBank/DDBJ databases. FT  
 CC -I- FUNCTION: Cytokine that stimulates the proliferation of T-lymphocytes. Stimulation by IL-15 requires interaction of IL-15 with components of IL-2R, including IL-2R beta and probably IL-2R gamma but not IL-2R alpha. FT  
 CC -I- SUBCELLULAR LOCATION: Secreted (IL15-S48AA). IL15-S21AA is not secreted, but rather is stored intracellularly, appearing in the nucleus and cytoplasmic components. FT  
 CC -I- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3; Name=IL15-S48AA; FT  
 CC IsoIa-P4-0933-1; Sequence=Displayed; FT  
 CC Name=IL15-S21AA; FT  
 CC IsoIa-P4-0933-2; Sequence=VSP\_002660; FT  
 CC Name=3'; FT  
 CC IsoIa-P4-0933-3; Sequence=VSP\_002661; FT  
 CC -I- TISSUE SPECIFICITY: Most abundant in placenta and skeletal muscle. It is also detected in the heart, lung, liver and kidney. IL15-S21AA is preferentially expressed in tissues such as testis and thymus. FT  
 CC -I- SIMILARITY: Belongs to the IL-15 family. FT  
 CC -I- DATABASE: NAME=R&D Systems, cytokine source book: IL15, CC  
 CC WWW="http://www.rndsystems.com/app/g\_sitebuilder.asp?bodyid=209". CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms> CC  
 CC Distributed under the Creative Commons Attribution-NonDerivs License CC  
 DR CC

RESULT 12

049528 HUMAN PRELIMINARY; PRT; 162 AA.

ID Q49528; HUMAN PRELIMINARY; PRT; 162 AA.

AC Q49528;

DT 13-SEP-2005, integrated into UniProtKB/T-EMBL.

DT 13-SEP-2005, sequence version 1.

DT 07-FEB-2006, entry version 2.

DR Interleukin 15, isoform 1.

GN Interleukin 15, isoform 1.

OS Homo sapiens (Human).

OC Homo sapiens (Human).

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OX NCBI\_TAXID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE OF 49-162. FT  
 RC TISSUE=PCO rescued clones; FT  
 MEDLINE=22382857; Published=2477932; DOI=10.1073/pnas.242603899; FT  
 RA Krausser R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., FT  
 RA Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., FT  
 RA Hopkins R.F., Jordan D., Moore T., Max S.I., Wang J., Hoile F., FT  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., FT  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., FT  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., FT  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., FT  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., FT  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., FT  
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A., FT  
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., FT  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., FT  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., FT  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., FT  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smilus D.E., FT  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., FT  
 RA "Generation and initial analysis of more than 15,000 full-length human FT  
 and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). FT  
 RL [2])

RN RP NUCLEOTIDE SEQUENCE OF 49-162. FT  
 RC TISSUE=PCO rescued clones; FT  
 RG NIH MGC Project; FT  
 RG Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases. FT  
 RL CC



RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klaubner R.D., Collins F.B., Wagner K.L., Schaefer C.M., Schuler G.D.,  
 RA Altenschul S.F., Zeeberg B.R., Buetow K.H., Schaeffer C.F., Bhattacharyya N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Maruskin B., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Bronstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rahe S.S., Loquellano N.A., Peters G.J.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McElvaney P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzy D.M., Soderberg B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,  
 RA Blasieley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalius D.E.,  
 RA Schnech A., Schein J.E., Jones S.J.M., Marr M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT RT and mouse cDNA sequences.", Proc Natl Acad Sci U S A, 99:1699-1603 (2002)

|                       |   |                                      |
|-----------------------|---|--------------------------------------|
| Qy                    | 12 RQLIDIVDQ---LNVYVNDLVPETI-PAPDVETNCMSA[PSCR]-----KQLKSA  | 13 3%; Score 94.5; DB 2; Length 160; |
| Best Local Similarity | 23 3%   | Pred. No. 1.2;                       |
| Matches               | 28;   | Mismatches                           |
|                       | Conservative  | 40;                                  |
|                       | Indels  | 27;                                  |
|                       | Gaps  | 5;                                   |
| Db                    | 48 RESVVKVQIAAKLNVNENDM-MYPTQANYK-[CKSKSTTCFAFEVSVLVB]QVESL | 105                                  |
| Qy                    | 60 NTGNRERITVSIKLRKRPSTNGRQRQHRLITCPSCDSYEKKPKPKEFRLFKSLQKM | 119                                  |
| Db                    | 106 AFROQJQILN-----RTVKDRKEMKPCVCELYKESTERKTFTLQHLEQM       | 152                                  |

Search completed: August 14, 2006, 21:51:42  
Job time : 304 secs

Job time : 304 secs

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